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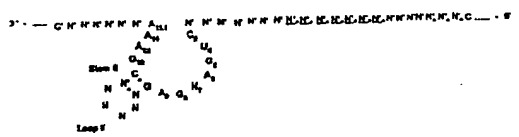
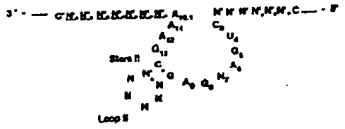
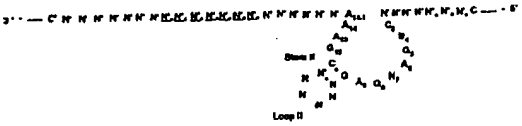
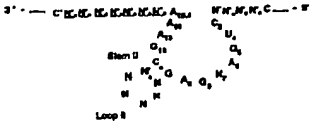

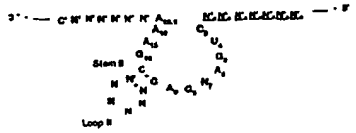

(57) Abstract

The invention features nucleic acid molecules with novel combinations of chemical modifications which are able to modulate gene expression.

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DESCRIPTION

Nucleic Acid Molecules With Novel Chemical Compositions Capable Of Modulating Gene Expression

This patent application relates to the patent application entitled, "NUCLEIC ACID MOLECULES WITH NOVEL CHEMICAL COMPOSITIONS CAPABLE OF MODULATING GENE EXPRESSION", U.S.S.N. 60/082,404, which was filed with the U.S. patent and trademark office on April 20, 1998. The earlier patent application listed Thompson *et al.* as inventors.

Background Of The Invention

This invention relates to novel chemically modified nucleic acid molecules that are capable of modulating gene expression through a variety of mechanisms. Specifically, the invention concerns novel combinations of chemical modifications in an oligonucleotide which enhance nuclease resistance, binding affinity, and/ or potency.

The following is a discussion of relevant art, none of which is admitted to be prior art to the present invention.

Since the discovery of the mechanisms underlying gene expression, specifically nucleic acid based transcription and translation, a great deal of effort has been placed on blocking or altering these processes for a variety of purposes, such as understanding biology, gene function, disease processes, and identifying novel therapeutic targets. Approaches involving nucleic acid molecules for modulating gene expression have gained popularity in recent years. For example, nucleic acid molecules have been designed which are capable of binding to specific mRNA sequences by Watson-Crick base pairing interaction and blocking translation (Crooke, 1996, *Medicinal Res. Rev.* 16, 319-344). Another approach involves complexation of DNA with triplex forming oligonucleotides to prevent transcription of bound DNA sequences thereby inhibiting gene expression (Kim *et al.*, 1998, *Biochemistry.* 37, 2299-2304). The interaction of antisense oligonucleotides, 2-5A antisense chimera, or ribozymes with target RNA have been used to prevent gene expression. All of these nucleic acid molecules are highly specific to their matching target sequences and therefore may offer lower toxicity compared to traditional approaches such as chemotherapy.

The use of oligonucleotides for modulation of gene expression generally requires stabilization of oligonucleotides from degradation by nucleases that are present in biological systems. Cellular efficacy may be effected if the nucleic acid molecule is

degraded before it reaches its desired target. Chemical modifications of nucleic acid molecules have been found to be advantageous in making them inaccessible to degradation by cellular nucleases. Uhlmann and Peyman, 1990, *Chem. Reviews* 90, 543, review the use of nucleoside modifications to stabilize antisense oligonucleotides. Besides improved stability, chemical modifications have also been shown to increase binding affinity, improve cellular penetration, and enhanced target specificity (Monia *et al.*, 1993, *J. Biol. Chem.* 268, 14514-14522; Wu-Pong, 1994, BioPharm, 22-33).

One of the most studied and utilized chemical alteration in oligonucleotides has been backbone modifications such as phosphorothioates. Phosphorothioate oligonucleotides are nucleic acid molecules whose phosphodiester linkage has been modified by substituting a sulfur atom in place of an oxygen atom. In addition to increased nuclease resistance, phosphorothioate oligonucleotides are substrates for ribonuclease H (RNase H) (Monia, *supra*; Crooke *et al.*, 1995, *Biochem. J.* 3112, 599-608). RNase H is an endonuclease which catalyzes the degradation of RNA in an RNA-DNA heteroduplex (Hostomsky *et al.*, 1993 in *Nucleases,* Linn *et al.*, eds., Cold Spring Harbor Laboratory Press, NY, 341-376). RNA/DNA heteroduplexes, called Okazaki fragments, are formed naturally during DNA replication. Therefore, the normal function of RNase H is to degrade the RNA portion of the heteroduplex to complete DNA replication. In experiments with *E. coli* RNase H, the phosphorothioate oligonucleotide activated the enzyme more efficiently (2-5 fold) compared to a standard phosphodiester containing oligonucleotide (Crooke, 1995, *supra*).

Binding of DNA to RNA is not as thermodynamically favorable as an RNA to RNA interaction (Altmann *et al.*, 1996, *Chimia* 50, 168-176). Inoe & Ohtsuka, 1987, *Nucleic Acids Research* 115, 6131, first proposed an oligonucleotide with a central region consisting of oligodeoxynucleotides flanked by 2'-*O*-methyl modified nucleotide regions. The region of oligodeoxynucleotides in such a chimeric molecule is recognized by RNase H when bound to target RNA; and facilitates cleavage of target RNA by RNase H. (Inoe & Ohtsuka, 1987, *FEBS* Lett. 215, 327; Shibahara & Morisava, 1987, *Nucleic Acids Res.* 15, 4403). Such chimeric oligonucleotides were proposed to interact with target RNA more stably than an all DNA oligonucleotide.

Subsequent developments included the introduction of nuclease resistant modifications of the chimeric oligonucleotides, such as methylphosphonates (Tidd & Gibson, 1988, *Anticancer Drug Design* 3, 117), phosphorothioates (Agrawal & Pederson, 1990, *Proc Nat. Acad. Sci. USA* 87, 1407), and phosphoramidates (Potts & Runyun, 1991, *Proc Nat. Acad. Sci. USA* 88, 1516). Additionally, the flanking sequences have been

modified with 2'-*O*-methyl and 2'-*F*-modifications (Cook, 1993, *Antisense Research and Applications*, CRC Press, 150-181).

Agrawal et al., US Patent No. 5,652,355, describe a phosphorothioate-containing nucleic acid molecule with at least two 2'-*O*-methyl modifications on the 5' and 3' ends.

Agrawal, US Patent No. 5,652,356, describes an oligonucleotide which consists of a region of 2'-*O*-substituted oligonucleotide located between two oligodeoxyribonucleotide regions. The DNA regions of this nucleic acid molecule consists of phosphorothioate modifications at every position.

Cook *et al.*, US Patent No. 5,623,065, describe the use of a nucleic acid molecule which contains an RNase H cleavable region flanked by certain specifically modified nucleotides, for inhibition of gene expression of a ras gene.

Cook *et al.*, US Patent No. 5,587,362, describe a nucleic acid molecule having "substantially chirally pure inter-sugar linkages", for modulation of gene expression.

Ohtsuka *et al.*, US Patent No. 5,013,830, describe mixed oligomers having a DNA region and a 2'-*O*-methyl modified region, useful for modulation of gene expression.

Walder *et al.*, US Patent No. 5,491,133, describe a method for modulating gene expression using chimeric oligonucleotides with 3'-phosphodiester linkage modifications.

Cohen *et al.*, US Patent No. 5,276,019, and Cohen *et al.*, US Patent No. 5,264,423 describe the use of oligodeoxynucleotides of no more than 32 nucleotides in length, containing at least one phosphorothioate internucleoside linkage which are capable of preventing foreign nucleic acid replication.

Cohen *et al.*, US Patent No. 5,286,717, describe an oligodeoxyribonucleotide with at least one phosphorothioate modification capable of inhibiting oncogenes.

Sproat *et al.*, US Patent No. 5,334,711, describe 2'-*O*-R modified hammerhead and hairpin ribozymes, where R IS ALKYL, ALKYNYL OR ALKENYL.

Crooke *et al.*, 1996, *Exp. Opin. Ther. Patents* 6, 855, list and discuss various patents and PCT publications in the field of antisense technology.

Sproat *et al.*, US Patent No. 5,678,731, describe 2'-*O*-R modified oligonucleotides where R IS ALKYL, ALKYNYL OR ALKENYL.

Usman *et al.*, US Patent No. 5,652,094, describe enzymatic nucleic acid molecules which include nucleic acid analogues or deoxyribonucleotides.

Joyce, International Publication No. WO 96/17086, describes a DNA enzyme capable of cleaving RNA.

Rossi *et al.*, US Patent No. 5,144,019, describe chimeric hammerhead ribozymes with the binding arms and stem II region modified with deoxyribonucleotides.

Molecules have also been devised which include non-nucleotides capable of binding to nucleic acid. These peptide nucleic acid (PNA) molecules bind by Watson-Crick base-pairing and may also function through an antisense mechanism. These molecules have been used to augment hammerhead ribozyme activity by altering the structure of target RNAs and increasing accessibility of cleavage sites (Jankowsky *et al.*, 1997, *Nucleic Acids Research* 25, 2690-2693).

Summary of the Invention

This invention relates to novel nucleic acid molecules which are useful for modulation of gene expression. The nucleic acid molecule of the instant invention are distinct from other nucleic acid molecules known in the art. Specifically, the nucleic acid molecules of the present invention have novel combinations of chemical modifications and are capable of binding to RNA or DNA to facilitate modulation of gene expression. These novel combinations of chemical modifications may be used to form antisense oligonucleotides, triplex forming oligonucleotides, 2-5A antisense chimera, and enzymatic nucleic acid molecules.

In a preferred embodiment, the invention features a nucleic acid molecule having the following formulae:

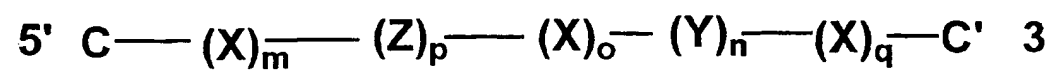
Formula I:

Formula II:

Formula III:

In a preferred embodiment, the invention features an enzymatic nucleic acid molecule having the formula:

Formula IV:



Formula V:

$$5'\ C\text{—}(X)_m\text{—}(Y)_n\text{—}(X)_o\text{—}(Z)_p\text{—}(X)_q\text{—}C'\ 3'$$

Formula VI:

$$5'\ C\text{—}(Y)_n\text{—}(Z)_p\text{—}(X)_q\text{—}C'\ 3'$$

Formula VII

$$5'\ C\text{—}(X)_q\text{—}(Z)_p\text{—}(Y)_n\text{—}C'\ 3'$$

In each of the above formula (I-VII), X represents independently a nucleotide which may be same or different; where m and o are integers independently greater than or equal to 4 and preferably less than about 100, more specifically 5, 6, 7, 8, 9, 10, 11, 12, 15, or 20; r is an integer greater than or equal to four, more specifically 5, 6, 7, 10, 15, or 20; the nucleic acid molecule may be symmetric (m =. O) or asymmetric (m O); $(X)_m$, $(X)_o$, and $(X)_q$ are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid molecule (the target can be an RNA, DNA or RNA/DNA mixed polymers); Y represents independently a deoxyribonucleotide which may be same or different; n is an integer greater than or equal to 4, specifically 5, 6 7, 8, 9, 10, 11, or 12; Z represents an oligonucleotide including nucleotides capable of facilitating the cleavage of a target sequence; p is of length greater than or equal to 4 but less than 100, preferably 5, between 10-20, specifically 25-55, specifically between 30-45, more specifically 35-50; q is an integer greater than or equal to 0, preferably 1, 2, 3, 4, 5, 6, 7, 8, 10, 15, 20; __ represents a chemical linkage (*e.g.* a phosphate ester linkage, amide linkage or others known in the art); and each $(X)_m$, $(X)_o$, $(X)_r$, $(X)_q$, and/or $(Y)_n$ independently comprise phosphorothioate linkages, more specifically each $(X)_m$, $(X)_o$, $(X)_r$, $(X)_q$, and/or $(Y)_n$ independently comprise at least one phosphodiester linkage and one phosphorothioate linkage; each C and C' independently represents a cap structure which may independently be present or absent; and $(Z)_p$ may optionally include a phosphorothioate linkage. The nucleotides in the each of the formula I-VII are unmodified or modified at the sugar, base, and/or phosphate as known in the art.

Preferably, each of X represents independently a nucleotide which may be same or different; where m and o are integers independently greater than or equal to 5; $(X)_m$ and $(X)_o$ are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid molecule; each $(X)_r$ comprises independently at least one phosphodiester linkage and one phosphorothioate linkage; Y represents independently a

deoxyribonucleotide which may be same or different; $(Y)_n$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule; n is an integer greater than or equal to 4; each $(X)_m$, and $(X)_o$ comprise independently at least one phosphodiester linkage and one phosphorothioate linkage; $(Y)_n$ comprises a phosphorothioate linkage or a phosphorodithioate linkage or a 5'-S-phosphorothioate, or 5'-S-phosphorodithioate, or a 3'-S-phosphorothioate or a 3'-S-phosphorodithioate linkage or a mixture thereof; and each C and C' independently represents a cap structure which may independently be present or absent.

By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a sugar moiety. Nucleotide generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see for example, Usman and McSwiggen, *supra*; Eckstein *et al.*, International PCT Publication No. WO 92/07065; Usman *et al.*, International PCT Publication No. WO 93/15187; Uhlman & Peyman, *supra*) all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art and has recently been summarized by Limbach *et al.*, 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into nucleic acids include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-methyluridine), propyne, and others (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090; Uhlman & Peyman, *supra*). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents; such bases may be used at any position, for example, within the catalytic core of an enzymatic nucleic acid molecule and/or in the substrate-binding regions of the nucleic acid molecule.

By "unmodified nucleotide" is meant a nucleotide with one of the bases adenine, cytosine, guanine, thymine, uracil joined to the 1' carbon of β-D-ribo-furanose.

By "modified nucleotide" is meant a nucleotide which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate.

By "sufficient length" is meant an oligonucleotide of greater than or equal to 4 nucleotides.

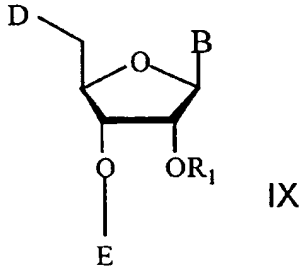
By "stably interact" is meant, interaction of the oligonucleotides with target nucleic acid (*e.g.*, by forming hydrogen bonds with complementary nucleotides in the target under physiological conditions). The interaction is stable either alone or in conjunction with $(Y)_n$ and $(Z)_p$ where applicable.

By "chimeric nucleic acid molecule" or "chimeric oligonucleotide" is meant that, the molecule may be comprised of both modified or unmodified DNA or RNA.

By "cap structure" is meant chemical modifications which have been incorporated at the terminus of the oligonucleotide. These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell.

In another preferred embodiment $(X)_m$, $(X)_o$, $(X)_q$, $(Y)_n$ and/or $(Z)_p$ independently include modifications selected from a group comprising 2'-*O*-alkyl (*e.g.* 2'-*O*-allyl; Sproat *et al., supra*); 2'-*O*-alkylthioalkyl (*e.g.* 2'-*O*-methylthiomethyl; Karpeisky *et al.*, 1998, *Nucleosides & Nucleotides* 16, 955-958); L-nucleotides (Tazawa *et al.*, 1970, *Biochemistry* 3499; Ashley, 1992, *J. Am. Chem. Soc.* 114, 9731; Klubmann *et al.*, 1996, Nature Biotech 14, 1112); 2'-*C*-alkyl (Beigelman *et al.*, 1995, *J. Biol. Chem.* 270, 25702); 1-5-Anhydrohexitol; 2,6-diaminopurine (Strobel *et al.*, 1994, *Biochem.* 33, 13824-13835); 2'-(*N*-alanyl) amino-2'-deoxynucleotide; 2'-(*N*-beta-alanyl) amino; 2'-deoxy-2'-(lysyl) amino; 2'-*O*-amino (Karpeisky *et al.*, 1995, *Tetrahedron Lett.* 39, 1131); 2'-deoxy-2'-(*N*-histidyl) amino; 5-methyl (Strobel, *supra*); 2'-(*N*-b-carboxamidine-beta-alanyl) amino; 2'-deoxy-2'-(N-beta-alanyl) (Matulic-Adamic *et al.*, 1995, *Bioorg. & Med. Chem. Lett.* 5,2721-2724); xylofuranosyl (Rosemeyer *et al.*, 1991, *Helvetica Chem. Acta,* 74, 748; Seela *et al.*, 1994, *Helvetica Chem. Acta,* 77, 883; Seela *et al.*, 1996, *Helvetica Chem. Acta,* 79, 1451).

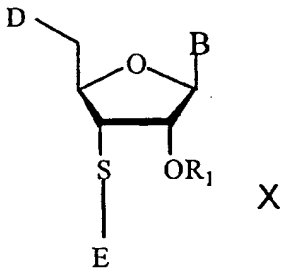
In a preferred embodiment, the invention features a nucleic acid molecule of any of formula I-VII, where each X and/or Z, independently include a nucleotide modification having formula IX:



IX

Where, each B is independently a modified or an unmodified nucleic acid base; R1 is independently a fluoroalkyl or an alkylthiofluoroalkyl; E is independently a phosphorus-containing group; and D is independently an O, blocking group or a phosphorus-containing group.

In another preferred embodiment, the invention features a nucleic acid molecule of any of formula I-VII, where each X and/or Z, independently include a nucleotide modification having formula X:



X

Wherein, each B is independently a modified or an unmodified nucleic acid base; R1 is independently an aklyl, an alkylthioalkyl, a fluoroalkyl or an alkylthiofluoroalkyl; E is independently a phosphorus-containing group; and D is independently an O, blocking group or a phosphorus-containing group.

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12 carbons. More preferably it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2 or $N(CH_3)_2$, amino, or SH. The term also includes alkenyl groups which are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2, halogen, $N(CH_3)_2$, amino, or SH. The term "alkyl" also includes alkynyl groups which have an unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When

substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2 or $N(CH_3)_2$, amino or SH.

Such alkyl groups may also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group which has at least one ring having a conjugated p electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above. Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

A "blocking group" is a group which is able to be removed after polynucleotide synthesis and/or which is compatible with solid phase polynucleotide synthesis.

A "phosphorus containing group" can include phosphorus in forms such as dithioates, phosphoramidites and/or as part of an oligonucleotide.

In yet another preferred embodiment C' is selected from a group comprising inverted abasic residue,. 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide, 4'-thio nucleotide, carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety (for more details see Beigelman *et al.*, International PCT publication No. WO 97/26270, incorporated by reference herein).

In yet another preferred embodiment C is selected from a group comprising, 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate;

hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moeity; 5'-5'-inverted abasic moeity; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moeities (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

In another preferred embodiment $(Z)_p$ includes a non-nucleotide linker. Thus, in a preferred embodiment, the invention features an enzymatic nucleic acid molecule having one or more non-nucleotide moieties, and having enzymatic activity to cleave an RNA or DNA molecule. By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine. The terms "abasic" or "abasic nucleotide" as used herein encompass sugar moieties lacking a base or having other chemical groups in place of base at the 1' position.

By the phrase "enzymatic nucleic acid" is meant a nucleic acid molecule capable of catalyzing (altering the velocity and/or rate of) a variety of reactions including the ability to repeatedly cleave other separate nucleic acid molecules (endonuclease activity) in a nucleotide base sequence-specific manner. Such a molecule with endonuclease activity may have complementarity in a substrate binding region (*e.g.* $(X)_m$, $(X)_o$, $(X)_q$ and $(Y)_n$ in formulae IV-VII) to a specified gene target, and also has an enzymatic activity that specifically cleaves RNA or DNA in that target. That is, the nucleic acid molecule with endonuclease activity is able to intramolecularly or intermolecularly cleave RNA or DNA and thereby inactivate a target RNA or DNA molecule. This complementarity functions to allow sufficient hybridization of the enzymatic RNA molecule to the target RNA or DNA to allow the cleavage to occur. 100% complementarity is preferred, but complementarity as low as 50-75% may also be useful in this invention. The nucleic acids may be modified at the base, sugar, and/or phosphate groups. The term enzymatic nucleic acid is used interchangeably with phrases such as ribozymes, catalytic RNA, enzymatic RNA, catalytic DNA, nucleozyme, DNAzyme, RNA enzyme, endoribonuclease, endonuclease, minizyme, leadzyme, oligozyme, chimeric ribozyme, chimeric enzymatic nucleic acid, or

DNA enzyme. All of these terminologies describe nucleic acid molecules with enzymatic activity.

By "complementarity" is meant a nucleic acid that can form hydrogen bond(s) with other RNA sequence by either traditional Watson-Crick or other non-traditional types (for example, Hoogsteen type) of base-paired interactions.

By "oligonucleotide" as used herein, is meant a molecule comprising two or more nucleotides.

By "enzymatic portion" is meant that part of the enzymatic nucleic acid molecule essential for cleavage of a nucleic acid substrate

By "substrate binding region" or "substrate binding domain" is meant that portion/region of a nucleic acid molecule (e.g. ribozyme) which is complementary to (*i.e.*, able to base-pair with) a portion of its substrate. Generally, such complementarity is 100%, but can be less if desired. For example, as few as 10 bases out of 14 may be base-paired. Such arms are shown generally in Figures 1 and 3. That is, in a ribozyme example, these arms contain sequences within a ribozyme which are intended to bring ribozyme and target RNA together through complementary base-pairing interactions. The ribozyme of the invention may have binding arms that are contiguous or non-contiguous and may be of varying lengths. The length of the binding arm(s) are preferably greater than or equal to four nucleotides; specifically 12-100 nucleotides; more specifically 14-24 nucleotides long. If two binding arms are chosen, the design is such that the length of the binding arms are symmetrical (*i.e.*, each of the binding arms is of the same length; *e.g.*, five and five nucleotides, six and six nucleotides or seven and seven nucleotides long) or asymmetrical (*i.e.*, the binding arms are of different length; *e.g.*, six and three nucleotides; three and six nucleotides long; four and five nucleotides long; four and six nucleotides long; four and seven nucleotides long; and the like).

By "DNAzyme" or "catalytic DNA" or "DNA enzyme" is meant, an enzymatic nucleic acid molecule lacking a 2'-OH group.

By "nucleic acid molecule" as used herein is meant a molecule comprising nucleotides. The nucleic acid can be composed of modified or unmodified nucleotides or non-nucleotides or various mixtures and combinations thereof.

In another preferred embodiment, the nucleic acid molecule of the present invention is conjugated with another moiety including but not limited to abasic nucleotides, polyether, polyamine, polyamides, peptides, carbohydrates, lipid, or polyhydrocarbon compounds. Those skilled in the art will recognize that these molecules may be linked to one or more of any nucleotides comprising the nucleic acid molecule at several positions on the sugar, base or phosphate group.

In yet another preferred embodiment, the nucleic acid molecule of the present invention can form structures including but not limited to antisense, triplexes, 2-5A chimera antisense, or enzymatic nucleic acid (ribozymes).

By "antisense" is meant a non-enzymatic nucleic acid molecule that binds to target RNA, for example, by means of RNA-RNA or RNA-DNA or RNA-PNA (protein nucleic acid; Egholm *et al.*, 1993 *Nature* 365, 566) interactions and alters the activity of the target RNA (for a review see Stein and Cheng, 1993 *Science* 261, 1004).

By "2-5A antisense chimera" it is meant, an antisense oligonucleotide containing a 5' phosphorylated 2'-5'-linked adenylate residues. These chimeras bind to target RNA in a sequence-specific manner and activate a cellular 2-5A-dependent ribonuclease which in turn cleaves the target RNA (Torrence *et al.*, 1993 *Proc. Natl. Acad. Sci. USA* 90, 1300).

By "triplex DNA" it is meant an oligonucleotide that can bind to a double-stranded DNA in a sequence-specific manner to form a triple-strand helix. Triple-helix formation has been shown to inhibit transcription of the targeted gene (Duval-Valentin *et al.*, 1992 *Proc. Natl. Acad. Sci. USA* 89, 504).

In another preferred embodiment, the invention features an antisense oligonucleotide which is capable of interacting with the target RNA and sterically blocking translation, where the oligonucleotide has a 5' and a 3' Cap structure and the oligonucleotide may include modifications at the base, sugar or the phosphate groups.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

Description of the Preferred Embodiments

The drawings will first briefly be described.

Drawings:

Figure 1 is a diagrammatic representation of a nucleic acid molecule with 7-9 phosphorothioate oligodeoxyribonucleotide sequence flanked by 9 non-deoxyribonucleotide containing oligonucleotides, binding to a target molecule.

Figure 2 displays schematic representations of certain chemical structures which may be incorporated into the nucleic acid molecule of the invention.

Figure 3 shows the secondary structure model for seven different classes of enzymatic nucleic acid molecules. Arrow indicates the site of cleavage. --------- indicate the target sequence. Lines interspersed with dots are meant to indicate tertiary interactions. - is meant to indicate base-paired interaction. **Group I Intron**: P1-P9.0 represent various stem-loop structures (Cech *et al.*, 1994, *Nature Struc. Bio.*, 1, 273). **RNase P (M1RNA)**:

EGS represents external guide sequence (Forster *et al.*, 1990, *Science*, 249, 783; Pace *et al.*, 1990, *J. Biol. Chem.*, 265, 3587). **Group II Intron:** 5'SS means 5' splice site; 3' SS means 3'-splice site; IBS means intron binding site; EBS means exon binding site (Pyle *et al.*, 1994, *Biochemistry*, 33, 2716). **VS RNA:** I-VI are meant to indicate six stem-loop structures; shaded regions are meant to indicate tertiary interaction (Collins, International PCT Publication No. WO 96/19577). **HDV Ribozyme:** : I-IV are meant to indicate four stem-loop structures (Been *et al.*, US Patent No. 5,625,047). **Hammerhead Ribozyme:** : I-III are meant to indicate three stem-loop structures; stems I-III can be of any length and may be symmetrical or asymmetrical (Usman *et al.*, 1996, *Curr. Op. Struct. Bio.*, 1, 527). **Hairpin Ribozyme:** Helix 1, 4 and 5 can be of any length; Helix 2 is between 3 and 8 base-pairs long; Y is a pyrimidine; Helix 2 (H2) is provided with a least 4 base pairs (*i.e.*, n is 1, 2, 3 or 4) and helix 5 can be optionally provided of length 2 or more bases (preferably 3 - 20 bases, *i.e.*, m is from 1 - 20 or more). Helix 2 and helix 5 may be covalently linked by one or more bases (*i.e.*, r is 1 base). Helix 1, 4 or 5 may also be extended by 2 or more base pairs (*e.g.*, 4 - 20 base pairs) to stabilize the ribozyme structure, and preferably is a protein binding site. In each instance, each N and N' independently is any normal or modified base and each dash represents a potential base-pairing interaction. These nucleotides may be modified at the sugar, base or phosphate. Complete base-pairing is not required in the helices, but is preferred. Helix 1 and 4 can be of any size (*i.e.*, o and p is each independently from 0 to any number, *e.g.*, 20) as long as some base-pairing is maintained. Essential bases are shown as specific bases in the structure, but those in the art will recognize that one or more may be modified chemically (abasic, base, sugar and/or phosphate modifications) or replaced with another base without significant effect. Helix 4 can be formed from two separate molecules, *i.e.*, without a connecting loop. The connecting loop when present may be a ribonucleotide with or without modifications to its base, sugar or phosphate. "q" is 2 bases. The connecting loop can also be replaced with a non-nucleotide linker molecule. H refers to bases A, U, or C. Y refers to pyrimidine bases. "____" refers to a covalent bond. (Burke *et al.*, 1996, *Nucleic Acids & Mol. Biol.*, 10, 129; Chowrira *et al.*, US Patent No. 5,631,359).

Figure 4 is a graph comparing cell proliferation rates of MCF-7 cells treatment with active and inactive ribozyme with mismatch arms targeted to estrogen receptor delivered with GSV transfection reagent. The sequence for the active ribozyme is given as Seq. ID. No.2725 and the inactive is 2726.

Figure 5 is a graph comparing RNA levels of c-raf RNA in PC-3 cells following treatment with antisense (Seq. ID. No 2717) and scrambled antisense (mismatch) controls.

Figure 6a and 6b displays several possible ribozymes comprising oligodeoxyribonucleotides. The symbols used in the diagram include: N' represents a nucleotide complementary to a nucleotide on the target molecule; N7 represents position 7 in the ribozyme molecule (Hertel, K. J., *et al.*, 1992, *Nucleic Acids Res.*, 20, 3252); N' represents a deoxyribonucleotide complementary to a nucleotide on the target molecule; s represents a phosphorothioate modification; C represents a chemical modification at the 5' end of the ribozyme; and C' represents a chemical modification at the 3' end.

Figure 7 shows examples of nucleotide modifications for incorporation into oligonucleotides.

Figure 8 is a graph demonstrating the level of c-raf mRNA in PC-3 cells following treatment with c-raf sequence targeting antisense nucleic acid molecules. The antisense molecules target regions within the intron/exon junction (Seq. I.D. Nos.2731-2735), intron (Seq. I.D. 2736) and exon (Seq. I.D. 2737). The results demonstrate the molecules' ability to inhibit c-raf mRNA compared to the untreated or mismatch control at two concentrations.

Figure 9 is a graph which demonstrates the ability of an antisense molecule represented by Seq. I.D. No. 2738 (phosphorothioate modifications at every deoxynucleotide position) to inhibit c-raf message in PC-3 cells over a period of five days compared to the untreated and mismatch controls at three different concentrations.

Figure 10 is a graph which demonstrates the ability of an antisense molecule represented by Seq. I.D. No. 2737 (three phosphorothoate modified nucleotides at both the 5' and 3' ends of the oligonucleotide) to inhibit c-raf message in PC-3 cells over a period of five days compared to the untreated control at three different concentrations.

Figure 11 is a graph which demonstrates the ability of an antisense molecule represented by Seq. I.D. No. 2744 (9 phosphorothioate modified DNA flanked by 7 2'-O-methylthiomethyl RNA nucleotides at the 5' and 3' end) to inhibit c-raf message in PC-3 cells over a period of five days compared to the untreated and mismatch control at three different concentrations.

Figure 12 is a graph showing the level of cellular proliferation inhibition exhibited by antisense oligonucleotides represented by Seq. I.D. Nos. 2738 and 2741. Also shown within the graph is the cellular proliferation after treatment of cells with a mismatch control (Seq. I.D. 2739).

Figure 13 is a graph showing the ability of oligonucleotides with different chemical modifications to inhibit c-raf mRNA. Each antisense molecule is compared to an untreated and mismatch control.

Figure 14 is a graph demonstrating a dose dependent inhibition of C-raf in PC-3 cells following treatment with antisense oligonucleotides (Seq. I.D. Nos. 2741 and 2738).

Figure 15 is a graph showing inhibition of bcl-2 mRNA by antisense oligonucleotides compared to untreated and mismatch controls.

Figure 16 is a graph showing the ability of several k-ras targeting antisense molecules to inhibit k-ras message

Figure 17 is a graph showing the ability of oligonucleotides with different chemical modifications to inhibit estrogen receptor mRNA. Each antisense molecule is compared to an untreated and mismatch control.

Figure 18 shows a scheme for the synthesis of 3'-deoxy-3'-thio guanosine nucleoside (scheme 1).

Figure 19 shows a scheme for the synthesis of S-(pyridyl-2-disulfanyl) derivative (scheme 2).

Figure 20 shows a scheme for the synthesis of 3'-deoxy-3'-thio guanosine phosphoramidite.

Figure 21 shows a scheme for the preparation of 5'-thio-nucleoside phosphoramidite and succinates.

Figure 22 shows a scheme for the synthesis of 3'-thio-2'-*O*-methyl uridine.

Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs (*e.g.*, antisense oligonucleotides, hammerhead or the hairpin ribozymes) are used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of RNA structure. The molecules of the instant invention were chemically synthesized. Oligodeoxyribonucleotides were synthesized using standard protocols as described in Caruthers *et al.*, 1992, *Methods in Enzymology* 211,3-19, and is incorporated by reference.

The method of synthesis used for normal RNA including certain enzymatic nucleic acid molecules follows the procedure as described in Usman *et al.*, 1987 *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990 *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684 and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale synthesis were conducted on a 394 Applied Biosystems, Inc. synthesizer using a modified 2.5 µmol scale protocol with a 5 min coupling step for alkylsilyl protected nucleotides and 2.5 min coupling step for 2'-*O*-

methylated nucleotides. Table II outlines the amounts, and the contact times, of the reagents used in the synthesis cycle. A 6.5-fold excess (163 μL of 0.1 M = 16.3 μmol) of phosphoramidite and a 24-fold excess of *S*-ethyl tetrazole (238 μL of 0.25 M = 59.5 μmol) relative to polymer-bound 5'-hydroxyl was used in each coupling cycle. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, were 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer; detritylation solution was 2% TCA in methylene chloride (ABI); capping was performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution was 16.9 mM I_2, 49 mM pyridine, 9% water in THF (Millipore). B & J Synthesis Grade acetonitrile was used directly from the reagent bottle. *S*-Ethyl tetrazole solution (0.25 M in acetonitrile) was made up from the solid obtained from American International Chemical, Inc.

Deprotection of the RNA was performed as follows. The polymer-bound oligoribonucleotide, trityl-off, was transferred from the synthesis column to a 4mL glass screw top vial and suspended in a solution of methylamine (MA) at 65 °C for 10 min. After cooling to -20 °C, the supernatant was removed from the polymer support. The support was washed three times with 1.0 mL of EtOH:MeCN:H_2O/3:1:1, vortexed and the supernatant was then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, were dried to a white powder.

The base-deprotected oligoribonucleotide was resuspended in anhydrous TEA•HF/NMP solution (250 μL of a solution of 1.5mL *N*-methylpyrrolidinone, 750 μL TEA and 1.0 mL TEA•3HF to provide a 1.4M HF concentration) and heated to 65°C for 1.5 h. The resulting, fully deprotected, oligomer was quenched with 50 mM TEAB (9 mL) prior to anion exchange desalting.

For anion exchange desalting of the deprotected oligomer, the TEAB solution was loaded onto a Qiagen 500® anion exchange cartridge (Qiagen Inc.) that was prewashed with 50 mM TEAB (10 mL). After washing the loaded cartridge with 50 mM TEAB (10 mL), the RNA was eluted with 2 M TEAB (10 mL) and dried down to a white powder.

Inactive hammerhead ribozymes were synthesized by substituting a U for G_5 and a U for A_{14} (numbering from Hertel, K. J., *et al.*, 1992, Nucleic Acids Res., 20, 3252).

The average stepwise coupling yields were >98% (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684).

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together by ligation (Moore *et al.*, 1992, *Science* 256,

9923; Draper *et al.*, International PCT publication No. WO 93/23569; Shabarova *et al.*, 1991, *Nucleic Acids Research* 19, 4247)

Administration of Nucleic Acid Molecules

Methods for the delivery of nucleic acid molecules is described in Akhtar *et al.*, 1992, *Trends Cell Bio.*, 2, 139; and *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995 which are both incorporated herein by reference. Sullivan *et al.*, PCT WO 94/02595, further describes the general methods for delivery of enzymatic RNA molecules . These protocols may be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, nucleic acid molecules may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of nucleic acid delivery and administration are provided in Sullivan *et al.*, supra and Draper *et al.*, PCT WO93/23569 which have been incorporated by reference herein.

The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a patient.

The negatively charged polynucleotides of the invention can be administered (*e.g.*, RNA, DNA or protein) and introduced into a patient by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention may also be formulated and used as tablets, capsules or elixirs for oral administration; suppositories for rectal administration; sterile solutions; suspensions for injectable administration; and the like.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, *e.g.*,

acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, *e.g.*, systemic administration, into a cell or patient, preferably a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation to reach a target cell (*i.e.*, a cell to which the negatively charged polymer is desired to be delivered to). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms which prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant *in* vivo systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes which lead to systemic absorption include, without limitations: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes expose the desired negatively charged polymers, *e.g.*, nucleic acids, to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation which can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach may provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as the cancer cells.

The invention also features the use of the a composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer an method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic *et al. Chem. Rev.* 1995, **95**, 2601-2627; Ishiwata *et al.*, *Chem. Pharm. Bull.* 1995, **43**, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic *et al.*, *Science* 1995, **267**, 1275-1276; Oku *et al.*,1995, *Biochim. Biophys. Acta*, **1238**, 86-90). The long-circulating liposomes enhance the

pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al.*, *J. Biol. Chem.* 1995, **42**, 24864-24870; Choi *et al.*, International PCT Publication No. WO 96/10391; Ansell *et al.*, International PCT Publication No. WO 96/10390; Holland *et al.*, International PCT Publication No. WO 96/10392; all of these are incorporated by reference herein). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen. All of these references are incorporated by reference herein.

The present invention also includes compositions prepared for storage or administration which include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985) hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents may be provided. *Id.* at 1449. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents may be used. *Id.*

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors which those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

Mechanism of action of Nucleic Acid Molecules of the Invention

Antisense: Antisense molecules may be RNA or DNA oligonucleotides and primarily function by specifically binding to matching sequences resulting in inhibition of peptide synthesis (Wu-Pong, Nov 1994, *BioPharm*, 20-33). The oligonucleotide binds to target RNA by Watson Crick base-pairing and blocks gene expression by preventing ribosomal translation of the bound sequences. Antisense molecules may also alter protein synthesis by interfering with RNA processing or transport from the nucleus into the cytoplasm (Mukhopadhyay & Roth, 1996, *Crit. Rev. in Oncogenesis* 7, 151-190).

In addition, binding of single stranded DNA to RNA may result in nuclease degradation of the heteroduplex (Wu-Pong, *supra*; Crooke, *supra*). To date, the only backbone modified DNA chemistry which will act as substrates for RNase H are phosphorothioates and phosphorodithioates. In experiments with *E. coli*, the oligodeoxyribonucleotides phosphorothioate modification activated RNase H more efficiently (2-5 fold) compared to the natural phosphodiester containing oligodeoxynucleotide (Crooke, 1995, *supra*). Applicant describes here for the first time that oligonucleotides with 5'-thiophosphate modification can activate RNase H cleavage of RNA.

Triplex Forming Oligonucleotides (TFO): Single stranded DNA may be designed to bind to genomic DNA in a sequence specific manner. TFOs are comprised of pyrimidine-rich oligonucleotides which bind DNA helices through Hoogsteen Base-pairing (Wu-Pong, *supra*)The resulting triple helix composed of the DNA sense, DNA antisense, and TFO disrupts RNA synthesis by RNA polymerase. The TFO mechanism may result in gene expression or cell death since binding may be irreversible (Mukhopadhyay & Roth, *supra*).

2-5A Antisense Chimera: The 2-5A system is an interferon mediated mechanism for RNA degradation found in higher vertebrates (Mitra *et al.*, 1996, *Proc Nat Acad Sci USA* 93, 6780-6785). Two types of enzymes, 2-5A synthetase and RNase L, are required for RNA cleavage. The 2-5A synthetases require double stranded RNA to form 2'-5' oligoadenylates (2-5A). 2-5A then acts as an allosteric effector for utilizing RNase L which has the ability to cleave single stranded RNA. The ability to form 2-5A structures with double stranded RNA makes this system particularly useful for inhibition of viral replication.

(2'-5')oligoadenylate structures may be covalently linked to antisense molecules to form chimeric oligonucleotides capable of RNA cleavage (Torrence, *supra*). These molecules putatively bind and active a 2-5A dependent RNase, the oligonucleotide/enzyme complex then binds to a target RNA molecule which can then be cleaved by the RNase enzyme.

Enzymatic Nucleic acid: Seven basic varieties of naturally-occurring enzymatic RNAs are known presently. In addition, several *in vitro* selection (evolution) strategies (Orgel, 1979, *Proc. R. Soc. London,* B 205, 435) have been used to evolve new nucleic acid catalysts capable of catalyzing cleavage and ligation of phosphodiester linkages (Joyce, 1989, *Gene,* 82, 83-87; Beaudry *et al.*, 1992, *Science* 257, 635-641; Joyce, 1992, *Scientific American* 267, 90-97; Breaker *et al.*, 1994, *TIBTECH* 12, 268; Bartel *et al.*,1993, *Science* 261:1411-1418; Szostak, 1993, *TIBS* 17, 89-93; Kumar *et al.*, 1995, *FASEB J.*, 9,

1183; Breaker, 1996, *Curr. Op. Biotech.*, 7, 442; Santoro *et al.*, 1997, *Proc. Natl. Acad. Sci.*, 94, 4262; Tang *et al.*, 1997, *RNA* 3, 914; Nakamaye & Eckstein, 1994, *supra*; Long & Uhlenbeck, 1994, supra; Ishizaka et al., 1995, *supra*; Vaish *et al.*, 1997, *Biochemistry* 36, 6495; all of these are incorporated by reference herein). Each can catalyze a series of reactions including the hydrolysis of phosphodiester bonds in *trans* (and thus can cleave other RNA molecules) under physiological conditions. Table I summarizes some of the characteristics of some of these ribozymes. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of an enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over other technologies, since the concentration of ribozyme necessary to affect a therapeutic treatment is lower. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base-pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can be chosen to completely eliminate catalytic activity of a ribozyme.

Nucleic acid molecules having an endonuclease enzymatic activity are able to repeatedly cleave other separate RNA molecules in a nucleotide base sequence-specific manner. Such enzymatic nucleic acid molecules can be targeted to virtually any RNA transcript, and efficient cleavage achieved *in vitro* (Zaug *et al.*, 324, *Nature* 429 1986 ; Uhlenbeck, 1987 *Nature* 328, 596; Kim et al., 84 *Proc. Natl. Acad. Sci. USA* 8788, 1987; Dreyfus, 1988, *Einstein Quart. J. Bio. Med.*, 6, 92; Haseloff and Gerlach, 334 *Nature* 585, 1988; Cech, 260 *JAMA* 3030, 1988; and Jefferies et al., 17 *Nucleic Acids Research* 1371, 1989; Santoro *et al.*, 1997 *supra*).

Because of their sequence-specificity, *trans*-cleaving ribozymes show promise as therapeutic agents for human disease (Usman & McSwiggen, 1995 *Ann. Rep. Med. Chem.* **30**, 285-294; Christoffersen and Marr, 1995 *J. Med. Chem.* **38**, 2023-2037). Ribozymes can be designed to cleave specific RNA targets within the background of cellular RNA. Such a cleavage event renders the RNA non-functional and abrogates protein expression

from that RNA. In this manner, synthesis of a protein associated with a disease state can be selectively inhibited.

Optimizing Ribozyme Activity

Catalytic activity of the ribozymes described in the instant invention can be optimized as described by Draper et al., *supra*. The details will not be repeated here, but include altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications (base, sugar and/or phosphate) that prevent their degradation by serum ribonucleases and/or enhance their enzymatic activity (see *e.g.*, Eckstein *et al.*, International Publication No. WO 92/07065; Perrault *et al.*, 1990 *Nature* 344, 565; Pieken et al., 1991 *Science* 253, 314; Usman and Cedergren, 1992 *Trends in Biochem. Sci.* 17, 334; Usman *et al.*, International Publication No. WO 93/15187; and Rossi *et al.*, International Publication No. WO 91/03162; Sproat, US Patent No. 5,334,711; and Burgin *et al., supra;* all of these describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of enzymatic RNA molecules). Modifications which enhance their efficacy in cells, and removal of bases from stem loop structures to shorten RNA synthesis times and reduce chemical requirements are desired. (All these publications are hereby incorporated by reference herein).

There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into enzymatic nucleic acid molecules without significantly effecting catalysis and with significant enhancement in their nuclease stability and efficacy. Ribozymes are modified to enhance stability and/or enhance catalytic activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-*C*-allyl, 2'-flouro, 2'-*O*-methyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992 *TIBS* 17, 34; Usman *et al.*, 1994 *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.*, 1996 *Biochemistry* 35, 14090). Sugar modification of enzymatic nucleic acid molecules have been extensively described in the art (see Eckstein *et al.*, *International Publication* PCT No. WO 92/07065; Perrault *et al. Nature* 1990, *344*, 565-568; Pieken *et al. Science* 1991, *253*, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.* 1992, *17*, 334-339; Usman *et al. International Publication* PCT No. WO 93/15187; Sproat, *US Patent* No. 5,334,711 and Beigelman *et al.*, 1995 *J. Biol. Chem.* 270, 25702; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into ribozymes without inhibiting catalysis, and are incorporated by reference herein. In view of such

teachings, similar modifications can be used as described herein to modify the nucleic acid catalysts of the instant invention.

Nucleic acid catalysts having chemical modifications which maintain or enhance enzymatic activity are provided. Such nucleic acid is also generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or *in vivo* the activity may not be significantly lowered. As exemplified herein such ribozymes are useful in a cell and/or *in vivo* even if activity over all is reduced 10 fold (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Such ribozymes herein are said to "maintain" the enzymatic activity on all RNA ribozyme.

Therapeutic ribozymes delivered exogenously must optimally be stable within cells until translation of the target RNA has been inhibited long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Clearly, ribozymes must be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of RNA (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677; incorporated by reference herein) have expanded the ability to modify ribozymes by introducing nucleotide modifications to enhance their nuclease stability as described above.

By "enhanced enzymatic activity" is meant to include activity measured in cells and/or *in vivo* where the activity is a reflection of both catalytic activity and ribozyme stability. In this invention, the product of these properties is increased or not significantly (less that 10 fold) decreased *in vivo* compared to an all RNA ribozyme.

In yet another preferred embodiment, nucleic acid catalysts having chemical modifications which maintain or enhance enzymatic activity is provided. Such nucleic acid is also generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or *in vivo* the activity may not be significantly lowered. As exemplified herein such ribozymes are useful in a cell and/or *in vivo* even if activity over all is reduced 10 fold (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Such ribozymes herein are said to "maintain" the enzymatic activity on all RNA ribozyme.

Inhibition Of Estrogen Receptor Gene Expression

Breast Cancer is one of the leading causes of death in women (Jiang and Jordan, 1992, *J. Natl. Cancer Inst.* 84, 580-591). There has been an intense effort to understand the molecular mechanisms for hormonal regulation of cell proliferation in breast cancer over the last several decades. It has been shown that many breast and endometrial cancers are dependent on estrogen for their growth and progression (Borras *et al*, 1994, *J. Steroid Biochem. Molec. Biol.* 48, 325-336). Estrogen receptor plays a pivotal role in these cancers

and thus controlling the expression of this gene is of paramount interest to researchers and clinicians. The estrogen receptor is a member of the steroid hormone receptor gene family that displays it's biological function as a ligand binding-dependent transcription factor. Tamoxifen is a nonsteroidal antiestrogen which treats all stages of breast cancer and may be used as a preventative compound in those predisposed to breast cancer (Jordan and Murphy, 1990, *Endocr. Rev.* 11; 578-610).

Most breast tumors are initially dependent upon estrogen for growth, and the estrogen receptor has been a key indicator for endocrine response, prognosis and survival from breast cancer. The MCF-7 human breast cancer cell line expresses high levels of estrogen receptor and is responsive to the effects of added estrogen (Borras *et al.*, 1996, *J. Steroid Biochem. Molec. Biol.* 57, 203-213; Pink and Jordan, 1996, *Cancer Res.* 56, 2321-2330). They are an excellent model system to study the effects of regulation of estrogen receptor in breast cancer. Ribozymes and antisense oligonucleotides represent a direct means of affecting the levels of estrogen receptor message. In estrogen dependent cell lines, decreased amounts of estrogen receptor transcript should lower overall amounts of estrogen receptor protein and prevent proliferation of those cells. The effects of estrogen receptor on sexual differentiation of brain has been examined using antisense oligonucleotides (McCarthy *et al.*, 1993 *Endocrinology* 133, 433-439). This application documents the effects of ribozymes and antisense oligonucleotides to estrogen receptor RNA levels and proliferation in MCF-7 cells.

Estrogen receptor may be inhibited using nucleic acid molecules, including the nucleic acid molecules of the present invention. Other references describe the use of antisense molecules to down regulate estrogen receptor RNA (Defazio *et al.*, 1997, *Cell Growth Differ.* 8, 903-911; Santagati *et al.*, 1997, *Mol. Endocrinol.* 11, 938-949; Williard *et al.*, 1994, *Gene* 149, 21-24; Jiang & Jordan, *supra*).

The nucleic acid molecules may be chemically synthesized and delivered using methods described above, or may be expressed within cells from eukaryotic promoters (*e.g.*, Izant and Weintraub, 1985 *Science* 229, 345; McGarry and Lindquist, 1986 *Proc. Natl. Acad. Sci.* USA 83, 399; Scanlon *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet *et al.*, 1992 *Antisense Res. Dev.*, 2, 3-15; Dropulic *et al.*, 1992 *J. Virol,* 66, 1432-41; Weerasinghe *et al.*, 1991 *J. Virol,* **65**, 5531-4; Ojwang *et al.*, 1992 *Proc. Natl. Acad. Sci. USA* 89, 10802-6; Chen *et al.*, 1992 *Nucleic Acids Res.*, 20, 4581-9; Sarver *et al.*, 1990 *Science* 247, 1222-1225; Thompson *et al.*, 1995 *Nucleic Acids Res.* 23, 2259; Good *et al.*, 1997, *Gene* Therapy, 4, 45; all of the references are hereby incorporated in their totality by reference herein). Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity

of such nucleic acids can be augmented by their release from the primary transcript by a ribozyme (Draper *et al.*, PCT WO 93/23569, and Sullivan *et al.*, PCT WO 94/02595; Ohkawa *et al.*, 1992 *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira *et al.*, 1991, *Nucleic Acids Res.*, 19, 5125-30; Ventura *et al.*, 1993 *Nucleic Acids Res.*, 21, 3249-55; Chowrira *et al.*, 1994 *J. Biol. Chem.* 269, 25856; all of the references are hereby incorporated in their totality by reference herein).

One type of nucleic acid molecules known as ribozymes, which can cleave target molecules, are expressed from transcription units (see for example Couture *et al.*, 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Ribozyme expressing viral vectors could be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. Preferably, the recombinant vectors capable of expressing the ribozymes are delivered as described above, and persist in target cells. Alternatively, viral vectors may be used that provide for transient expression of ribozymes. Such vectors might be repeatedly administered as necessary. Once expressed, the ribozymes cleave the target mRNA. The active ribozyme contains an enzymatic center or core equivalent to those in the examples, and binding arms able to bind target nucleic acid molecules such that cleavage at the target site occurs. Other sequences may be present which do not interfere with such cleavage. Delivery of ribozyme expressing vectors could be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that would allow for introduction into the desired target cell (for a review see Couture *et al.*, 1996, *TIG.*, 12, 510).

In one aspect the invention features, an expression vector comprising nucleic acid sequence encoding at least one of the nucleic acid molecules of the instant invention is disclosed. The nucleic acid sequence encoding the nucleic acid catalyst of the instant invention is operable linked in a manner which allows expression of that nucleic acid molecule.

In another aspect the invention features, the expression vector comprises: a transcription initiation region (*e.g.*, eukaryotic pol I, II or III initiation region); b) a transcription termination region (*e.g.*, eukaryotic pol I, II or III termination region); c) a gene encoding at least one of the nucleic acid catalyst of the instant invention; and wherein said gene is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. The vector may optionally include an open reading frame (ORF) for a protein operably linked on the

5' side or the 3'-side of the gene encoding the nucleic acid catalyst of the invention; and/or an intron (intervening sequences).

Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990 *Proc. Natl. Acad. Sci. U S A*, 87, 6743-7; Gao and Huang 1993 *Nucleic Acids Res.*, 21, 2867-72; Lieber et al., 1993 *Methods Enzymol.*, 217, 47-66; Zhou et al., 1990 *Mol. Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that ribozymes expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet et al., 1992 *Antisense Res. Dev.*, 2, 3-15; Ojwang et al., 1992 *Proc. Natl. Acad. Sci. U S A*, 89, 10802-6; Chen *et al.*, 1992 *Nucleic Acids Res.*, 20, 4581-9; Yu et al., 1993 *Proc. Natl. Acad. Sci. U S A*, 90, 6340-4; L'Huillier *et al.*, 1992 *EMBO J.* 11, 4411-8; Lisziewicz *et al.*, 1993 *Proc. Natl. Acad. Sci. U. S. A.*, 90, 8000-4; Thompson *et al.*, 1995 *Nucleic Acids Res.* 23, 2259; Sullenger & Cech, 1993, *Science*, 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as ribozymes in cells (Thompson *et al., supra*; Couture and Stinchcomb, *1996, supra*; Noonberg *et al.*, 1994, *Nucleic Acid Res.*, 22, 2830; Noonberg *et al.*, US Patent No. 5,624,803; Good *et al.*, 1997, *Gene Ther.* 4, 45; Beigelman *et al.*, International PCT Publication No. *WO 96/18736*; all of these publications are incorporated by reference herein. The above ribozyme transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, *1996, supra)*.

In yet another aspect the invention features an expression vector comprising nucleic acid sequence encoding at least one of the catalytic nucleic acid molecule of the invention, in a manner which allows expression of that nucleic acid molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; c) a gene encoding at least one said nucleic acid molecule; and wherein said gene is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic

acid molecule. In another preferred embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; d) a gene encoding at least one said nucleic acid molecule, wherein said gene is operably linked to the 3'-end of said open reading frame; and wherein said gene is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In yet another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) a gene encoding at least one said nucleic acid molecule; and wherein said gene is operably linked to said initiation region, said intron and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; e) a gene encoding at least one said nucleic acid molecule, wherein said gene is operably linked to the 3'-end of said open reading frame; and wherein said gene is operably linked to said initiation region, said intron, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

Target Validation

One of the most challenging tasks in drug discovery is the choice of a therapeutic target. Historically, traditional biochemical and other studies have offered limited information in this regard. However, recent advances in genomics offer the potential to revolutionize both the speed and certainty of therapeutic target identification. Progress in characterizing the genes in the human genome has been very rapid, and it is now estimated that the entire complement of genes in the human genome may be sequenced before the end of this century. However, this mass of information is coming to the scientific world without a road map. Converting pure gene sequence information into a functional understanding of their role in human disease is proving to be a much more difficult problem. Even after a group of genes is associated with a particular disease, the process of validating which genes are appropriate for use as therapeutic targets is often slow and costly. Most companies with genomics activities now have access to myriad partial or full sequences, but do not possess adequate technologies to determine which of those sequences is an appropriate therapeutic target. As a result, only a few genes have been unequivocally identified as the causative agent for a specific disease.

The nucleic acid molecules of the present invention can inhibit gene expression in a highly specific manner by binding to and causing the cleavage of the mRNA

corresponding to the gene of interest, and thereby prevent production of the gene product (Christoffersen, *Nature Biotech,* **1997**, 2, 483-484). Appropriate delivery vehicles can be combined with these nucleic acid molecules (including polymers, cationic lipids, liposomes and the like) and delivered to appropriate cell culture or *in vivo* animal disease models as described above. By monitoring inhibition of gene expression and correlation with phenotypic results, the relative importance of the particular gene sequence to disease pathology can be established. The process may be both fast and highly selective, and allow for the process to be used at any point in the development of the organism. The novel chemical composition of these nucleic acid molecules may allowed for added stability and therefore increased efficacy.

Examples

The following are non-limiting examples demonstrating the utility of the nucleic acid molecules of the instant invention. Those in the art will recognize that certain experimental conditions such as temperatures, reaction times, media conditions, transfection reagents and RNA assays are not meant to be limiting and can be readily modified without significantly altering the protocols.

Example 1: Identification of Potential Nucleic Acid Molecule Binding Sites

The sequences of target RNAs were screened for accessible sites using a computer folding algorithm. Regions of the mRNA that did not form secondary folding structures were identified. For ribozyme sites, regions of mRNA that did not form secondary structure and contained potential hammerhead and/or haripin cleavage sites were identified.

Example 2: Selection of Ribozyme Cleavage Sites in Estrogen Receptor RNA

To test whether the sites predicted by the computer-based RNA folding algorithm corresponded to accessible sites in estrogen receptor. Ribozyme target sites were chosen by analyzing genomic sequences of Genbank Sequence HSERRI (Green *et al.*, 1986, *Nature* 320, 134-139) and prioritizing the sites on the basis of folding. Ribozymes were designed that could bind each target (see Figure 3) and were individually analyzed by computer folding (Christoffersen *et al.*, 1994 *J. Mol. Struc. Theochem,* 311, 273; Jaeger *et al.*, 1989, *Proc. Natl. Acad. Sci. USA*, **86**, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core were eliminated from consideration. As noted below, varying binding arm lengths can be

chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA. Hammerhead (Seq. ID. Nos.1-1245) and hairpin ribozymes (2491-2603) are listed in tables IV and V respectively.

Example 3: Inhibition of c-raf RNA Targets using Nucleic Acid Molecules

Prostate cancer cells (PC-3) were grown in a growth media consisting of Kaighn's F-12K media, 10% FBS, 1% glutamine, 20 mM HEPES, and 1% pen/strep to sub-confluent densities. A 4X concentration (10 μg/mL) of GSV (Glen Research) was prepared from a 2 mg/mL stock solution as well as a 10μM solution of antisense and its scrambled (mismatch) control. Complexes of antisense and GSV were formed in a 96 well plate by channel pipetting in antisense and GSV to form complex solutions which are twice the final concentrations. 50 μL of the complex solution and 50 μL of growth medium (without antibiotics) were added to PC-3 cells and incubated for 24 hours. The final concentrations of antisense used were 400, 200, and 100 nM, while the GSV concentration was held constant at 2.5 μg/mL. PC-3 cells were then harvested with 150 μL of RLT lysis buffer (Qiagen). RNA was purified using Qiagen's instructions and RNA was quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. The c-raf RNA concentration was normalized to the c-raf RNA concentrations of the scrambled controls. The antisense sequence (Seq. I.D. No. 2717) and the data is shown in table IIIA and figure 5. The antisense molecules were capable of reducing c-raf RNA levels up to 80% compared to the mismatch control in PC-3 cells at several concentrations of antisense molecules.

Example 4: Ribozyme *in vitro* Cleavage Assay

Ribozymes and complementary substrates were synthesized as described above. These ribozymes can be tested for cleavage activity *in vitro*, for example using the following procedure. The ribozyme sequences are shown in figure 7.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for ribozyme cleavage assay was prepared by *in vitro* transcription in the presence of [a-^{32}P] CTP, passed over a G 50 Sephadex column by spin chromatography and used as substrate RNA without further purification. Alternately, substrates may by 5'-^{32}P-end labeled using T4 polynucleotide kinase enzyme. Assays were performed by pre-warming a 2X concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5 at 37°C, 10 mM $MgCl_2$) and the cleavage reaction was initiated by adding the 2X ribozyme mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also pre-warmed in cleavage buffer. The assays were carried out for 1 hour at 37°C using a

final concentration of either 1 μM ribozyme, *i.e.*, ribozyme excess. The reaction was quenched by the addition of an equal volume of 95% formamide, 20 mM EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample was heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage were visualized on an autoradiograph of the gel. The percentage of cleavage was determined by Phosphor Imager® quantitation of bands representing the intact substrate and the cleavage products. The ribozymes were able to cleave between 1-80.8% of their complementary substrates after 2 hours (table VI).

Example 5: Inhibition of Cell Proliferation Using Estrogen Receptor Targeted Ribozyme

MCF-7 cells were were grown in a T-75 flask to 80% confluency in growth media, which was prepared by mixing 500 mL Alpha-MEM, 10 mL 1M Hepes, 5mL sodium Pyruvate, 5 mL NEAA, 5 mL L-glutamine, 250 μL 2.0 mg/ml insulin, 500 μl Gentamycin, and 10% FBS following by sterile filtration.

Ribozyme and cationic lipid was mixed as described in example 4 with final concentrations of 20, 40, and 80 nM ribozyme and 1 μg/mL GSV. The MCF-7 cells were treated with serum free alpha-MEM 24 hours prior to exposure to ribozyme/transfection reagent complexes. The complexes were added to the cells and allowed to continously transfect for 1,2 , 3, 4, and 5 days. At the end of each time point, the media was removed off the cells and proliferation was measured using a CyQuant kit (Molecular Probes). Fluorescence was measured at after 10 minutes of incubation at 485 nm (excitation) and 538 (emission). Inhibition of cellular proliferation by active ribozyme was compared to inactive scrambled ribozyme controls. The sequence for the active ribozyme is given as sequence ID. No. 2725 and the inactive scrambled control is given as Seq. ID. No. 2726. The chimeric enzymatic nucleic acid was able to inhibit MCF-7 cellular proliferation at all of the tested concentrations (figure 4).

Example 6: Inhibition of Estrogen Receptor RNA Targets using antisense nucleic acid molecules

A 5X concentrated solution of oligonucleotide (1μM) and a 10X solution of GSV (25 μg/mL) (Glen Research) was made prior to complexing. The 5X oligonucleotide solution (8 μL), 10X GSV solution (40 μL), and Optimem media (32 μL) were mixed together and incubated at 37°C for 15 minutes. Media was aspirated off the cells followed by the addition of 80 μL of fresh growth media (Optimem media with 10% FBS, 1% non-essential amino acids, 1% sodium pyruvate, 20mM HEPES, 1 μg/mL insulin) and 20 μL

of 5X complex solution. The complex was left on the cells for 20 hours and then harvested with 150 µL of RLT lysis buffer (Qiagen). RNA levels were then quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. This cellular delivery assay was used for several RPI targets in varying cell lines and the data is shown in table IIIA. The levels of target RNA were either normalized to mismatch control RNA or to an internal housekeeping gene such as actin. Antisense nucleic acid molecules, which are given as Seq. ID. Nos. 2718-2723, were able to knock down estrogen receptor RNA by varying degrees. The levels of RNA inhibition ranged from 48-64% depending on the antisense sequence.

Example 7: Inhibition of Estrogen Receptor RNA using Ribozymes

Ribozymes and GSV transfection reagents were mixed together using a protocol similar to the one found in example 6. Target RNA was purified using a Qiagen kit. RNA levels were then quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. The ribozyme specific to estrogen receptor is given as sequence ID. No. 2724 and was able to inhibit the gene by 50%.

Example 8: Inhibition of c-Raf mRNA and Cellular Proliferation Using Antisense Nucleic Acid Molecules

24 Hour RNA endpoint assay: The effect of targeting intron, exon, and intron-exon junction sites with antisense molecules was tested on c-raf RNA using *in vitro* cell culture assays. Seven chimeric antisense oligonucleotides with various chemical modifications were tested and the results were compared to an untreated control and an oligonucleotide modified at every nucleotide position with a phosphorothioate modification. Prostate cancer cells (PC-3) were grown in growth media consisting of Kaighn's F-12K media, 10% FBS, 1% glutamine, 20 mM HEPES, and 1% pen/strep in 96 well plates (15,000 cells per well). For the 24 hour delivery experiments, 2.5 mg/mL of GSV transfection reagent (Glen Research) was complexed to either 200 or 400 nM concentration of antisense molecules. The complex was left on the cells for 24 hours and the cells were then harvested with 150 µL of RLT lysis buffer (Qiagen). RNA levels were quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. C-raf RNA levels were normalized to actin controls and the data is shown in Figure 8. All compounds demonstrated an ability to inhibit c-raf message. Of the compounds tested, sequence I.D. 2732, 2736 and 2737 seemed particularly effective.

Sustained delivery RNA endpoint assay: Prostate cancer cells (PC-3) were grown in growth media consisting of Kaighn's F-12K media, 10% FBS, 1% glutamine, 20 mM

HEPES, and 1% pen/strep in 96 well plates (15,000 cells per well). The cells were plated to 2500 cells per well in a 96 well plate and incubated at 37°C. Antisense nucleic acid molecules (Seq. I.D. Nos. 2738, 2737, 2744; Table IV) and GSV transfection reagent were complexed as in described under example 4 to a final concentration of antisense molecules of 100, 200 or 400 nM with 1.0 μg/mL of GSV transfection reagent. For seq. I.D. No. 2744, a mismatch control with similar base composition was also tested as a control. The complex was left on the cells and allowed to continuously transfect for 1, 3, or 5 days. At the end of each time period, the cells were harvested with 150 μL of RLT lysis buffer (Qiagen); and RNA levels quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. The inhibition of c-raf expression by molecules represented by Seq. I.D. Nos. 2738, 2737, and 2744 (table IV) are shown in Figures 9, 10, and 11 respectively. All three of these molecules demonstrated the ability to reduce c-raf RNA between 60-90% compared to the untreated control.

Proliferation Assay: Chimeric oligonucleotides and delivery reagents were mixed as described in example 6 where the final concentration of antisense oligonucleotide is 200 nM (Seq. I.D. No.2738 and 2741) and GSV is 1 μg/mL. A mismatch antisense control was also tested (Seq. I.D. No. 2739) in this experiment. The MCF-7 cells were treated with serum free alpha-MEM 24 hours prior to exposure to antisense/transfection reagent complexes. The complexes were added to the cells and allowed to continuously transfect for 1, 3, or 5 days. At the end of each time point, the media was removed off the cells and proliferation was measured using a CyQuant kit (Molecular Probes). Fluorescence was measured after 10 minutes of incubation at 485 nm (excitation) and 538 (emission). Inhibition of cellular proliferation by active oligonucleotide was compared to scrambled mismatch controls. The antisense molecules targeting c-raf mRNA were able to inhibit cellular proliferation by up to 55%.

Varying Chemical Modifications: Referring to Figure 13 and Table IV, alterations of the chemical composition of antisense molecules were made while keeping the oligonucleotide sequence constant. All of the sequences were the same except for the mismatch controls and Seq. I.D. Nos. 2738 and 2739 (table IV) which were two nucleotides shorter than the others. Antisense molecules and GSV transfection reagent were mixed using the protocol described under example 6. The complexes were added to the cells and allowed to continuously transfect for 24 hours. The cells were then harvested with 150 μL of RLT lysis buffer (Qiagen). RNA levels were then quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. All c-raf levels were normalized using actin RNA as a control. Referring to Figure 13,

antisense molecules which utilized phosphorothioate modifications, inverted abasic caps, 2'-*O*-methyl or 2'-*O*-methylthiomethyl modifications inhibit c-raf mRNA.

Dose dependent Inhibition: 0, 50, 100 150, and 200 nM of antisense molecules (seq. I.D. No. 2738 or 2737) were mixed with mismatch control antisense molecules to give a final antisense/mismatch antisense concentration of 200nM for each sample. The antisense nucleic acid and GSV were complexed as in example 6 with a final GSV transfection reagent concentration at 2.5 μg/mL. The complexes were added to the cells and allowed to continuously transfect for 24 hours. At the end of each time period, the cells were harvested with 150 μL of RLT lysis buffer (Qiagen). RNA levels were then quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. All c-raf levels were normalized using actin RNA as a control. The results (Figure 14) show that c-raf is inhibited in a dose dependent manner and that the IC50 is approximately 35 nM for each of the antisense molecules.

Example 9: Ribonuclease Protection Assay of MCF-7 Cells treated with Antisense Nucleic Acid Molecules Targeting BCL-2

MCF-7 cells were plated in RPMI 1640 (10% FBS, 1% l-glutamine, 20 mM HEPES) at 100,000 cells per well for 24 hours. On the following day, the cells were treated with 150 nM of antisense nucleic acid molecules (Seq. I.D. Nos. 2749-2753; Table VIII) complexed with 5.4 μM of LipofectAMINE (LFA) for 4 hours. The antisense/LFA complex was then aspirated off and fresh RPMI 1640 media was added to the cells. 24 hours later the cells were harvested using RLT lysis buffer (Qiagen). A ribonuclease protection assay (Ambion) was then performed using the manufacturers protocol to quantitate RNA levels and then harvested with 150 μL of RLT lysis buffer (Qiagen). RNA levels were then quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. Bcl-2 RNA levels were normalized to GAPDH controls and is shown in Figure 15. The antisense oligonucleotides specifically inhibited Bcl-2 expression in MCF-7 cells.

Example 10: Inhibition of k-ras in DLD-1 Cells

96-well plates with DLD-1 cells at 10,000 cells per well were plated in complete RPMI 1640 media ((10% FBS, 1% l-glutamine, 20 mM HEPES, 1% pen/strep). Antisense molecules (Seq. I.D. Nos. 2754-2757; Table VIII) were complexed with GSV transfection reagent (Glen Research) using the method described in example 6. The final concentrations delivered to the cells were 200 nM antisense oligonucleotide and 1.25 μg/mL of GSV. The complex was added to the cells for 26 hours and at the end of the

time period, the cells were harvested with 150 µL of RLT lysis buffer (Qiagen). RNA levels were then quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. All k-ras levels were normalized using actin RNA as a control. The data (Figure 16) demonstrates that the antisense molecules can inhibit approximately 50-90% k-ras expression compared to the untreated or mismatch controls.

Example 11: Inhibition of Estrogen Receptor mRNA Using Antisense Molecules of varying Chemical Composition

Alteration of the chemical composition of antisense molecules were made while keeping the oligonucleotide sequence constant. All of the sequences (Table VII: Seq. I.D. Nos. 2758, 2760, 2762, 2764, 2766, 2768) were the same except for the mismatch controls (Table VII: Seq. I.D. Nos. 2759, 2761, 2763, 2765, 2767, 2769). Antisense molecules and GSV transfection reagent was mixed using the protocol described in example 6. The complexes were added to MCF-7 cells and allowed to continuously transfect for 24 hours. The cells were harvested with 150 µL of RLT lysis buffer (Qiagen). RNA levels were then quantified using Taqman reagents and the 7700 Prism (Perkin Elmer) using the manufacturer's protocol. All estrogen receptor mRNA levels were normalized using actin RNA as a control. The antisense molecules which included phosphorothioate modifications, inverted abasic caps, 2'-*O*-methyl or 2'-*O*-methylthiomethyl modifications appeared to decrease estrogen receptor RNA (Figure 17).

Example 12: Synthesis of 3'-deoxy-3'-thio Guanosine and it's 3'-Thiophosphoramidite

Referring to **Figures 18,** Applicant has developed an efficient method for the synthesis of 3'-deoxy-3'-thio guanosine **(13)** and its 3'-thiophosphoramidite **23** from guanosine. Reaction of suitably protected guanosine with a-acetoxyisobutyryl bromide (a-AIBBr) afforded stereoselectively 3'-deoxy-3'-bromo-2'-*O*-acetyl-b-D-xylofuranosyl derivative **3** which was converted into the 7:3 mixture of *S*-acyl ribofuranosyl derivatives **5** (or **6**) and 3',4'-unsaturated derivative **4**. *S*-acylated derivatives **5** and **6** were then converted in three steps into 3'-deoxy-3'-*S*-pyridylsulfanyl-5'-*O*-(4,4'-dimethoxytrityl)guanosine **(11)** which served as a common intermediate for the preparation of free nucleoside **13** and 3'-thiophosphoramidite **23.**

Oligonucleotides containing 3'-*S*-phosphorothiolate linkage have attracted increasing interest as probes for studying the interaction of nucleic acids and their processing enzymes. In particular these analogs have been used in revealing the involvement of metal ions in phosphoester transfer reactions catalyzed by RNA (Piccirilli *et al., J. Am. Chem. Soc.* **1996,** *118,* 10341) and ribonucleoprotein enzymes (Sontheimer

et al., Nature **1997**, *308*, 801). The synthesis of 3'-*S*-phosphorothiolate linked deoxyribodinucleotides have been reported using solution chemistry and solid phase chemistry (Cosstick *et al., Nucleic Acids. Res.* **1990**, *18*, 829; Li *et al., Tetrahedron* **1992**, *48*, 2729; Li *et al., J. Chem. Soc. Perkin Trans. 1* **1994**, 2123; Vyle *et al., Biochemistry* **1992, 31**, 3012).

The synthesis of ribonucleotide 3'-*S*-phosporothiolate analogs has been limited to the preparation of UspU (Liu *et al., Tetrahedron Lett.* **1996**, *37*, 925) and IspU (Weinstein *et al., J. Am. Chem. Soc.* **1996**, *118*, 10341) dimers using solution chemistry. Recently, Sun *et al.* (*RNA* **1997**, *3*, 1352) described direct incorporation of 3'-*S*-phosphorothioamidites into RNA using standard phosphoramidite solid phase synthesis.

One general approach to the synthesis of 3'-thio ribonucleosides involves preparation of 3-thio ribose derivative, followed by the attachment of the desired nucleoside base (Ryan *et al., J. Org. Chem.* **1968**, *33*, 1783; Cao, *et al., Bioorg. Med. Chem. Lett.* **1994**, *4*, 807). While glycosylation reactions using pyrimidines proceed in high yields, purine bases generally give more complex mixtures because both N-7 and N-9 of the purine base are reactive towards glycosylation. Sun *et al., supra,* reported the first synthesis of 3'-thio guanosine derivatives using the above described approach. Coupling of per-acylated 3'-thioribose with persilylated N^2-acetylguanine proceeded in ca 40% yield and subsequent synthetic steps proceeded in a low overall yield.

Synthesis of 3'-thio adenosine (Mengel, *et al., Tetrahedron Lett.* **1977**,1177), 3'-thio uridine (Liu *et al., 1996 supra)* and 3'-thio inosine (Higson *et al., Tetrahedron* **1996**, *52*, 1027) all starting from preformed nucleosides are also reported.

Applicant describes a novel and improved process for the synthesis of 3'-deoxy-3'-thio guanosine (**13**) and its phosphoramidite **23** from guanosine as a starting material. It was recently reported (He *et al., Tetrahedron Lett.* **1995**, *39*, 6991) that the reaction of N^2-(dimethylaminomethylene)-guanosine **1** with a-AIBBr (the Mattocks-Moffatt reagent; Russell *et al., J. Am. Chem. Soc.* **1973**,*95*, 4025) proceeded stereoselectively yielding exclusively 3'-bromo-3'-deoxy-b-D-xylofuranosyl derivative. In general, reactions of base-unprotected purine nucleosides with this reagent result in the mixtures of trans bromo acetates of xylo- and arabino- configuration. Applicant used this reaction on the suitably 5'-protected N^2-(dimethylaminomethylene)guanosine derivative **2** (Scheme 1; **Figure 18**). 5'- protection in **2** helps to reduce the complexity of reaction products by eliminating possible formation of the mixture of 5'-OH, 5'-(2,5,5-trimethyl-1,3-dioxolan-4-on-yl) and/or 5'-*O*-acylated derivatives in reaction with a-AIBBr. This way, identification of the reaction products becomes straightforward. Applicant has chosen the *t*-butyldiphenylsilyl (TBDPS) protection because of its relatively high stability towards acidic conditions

required during the reaction with a-AIBBr in moist acetonitrile. This group is also expected to undergo selective cleavage in the presence of *S*-acyl groups. Reaction of **1** with TBDPS-Cl proceeded quantitatively to afford the 5'-*O*-silyl derivative **2** which reacted smoothly with a-AIBBr yielding the desired 3'-bromo-3'-deoxy-b-D-xylofuranosyl derivative **3** in a high yield. Reaction of **3** with potassium thioacetate or potassium thiobenzoate yielded the 3'-*S*-Ac or 3'-*S*-Bz derivatives **5** and **6**, respectively, along with 3',4'-unsaturated derivative **4**. The latter is formed by competing elimination reaction. The ratio was 7:3 in favor of the substitution products **5** and **6** which could not be separated from the elimination product **4** at this stage. The mixture of **4** and **5** (or **4** and **6**) was treated with tetrabutylammonium fluoride (TBAF) buffered with an excess of acetic acid; following chromatographic separation the desired 5' de-protected derivative **7** was obtained in a good yield. The unsaturated derivative **4** was unstable under the acidic reaction conditions and could not be isolated in a pure state by silica gel column chromatography. When triethylamine trihydrofluoride (TEA•3HF) reagent was used for deprotection, desilylation did not proceed to completion.

It is desirable to keep guanosine derivatives protected with lipophylic groups during synthetic transformations because of the solubility problems encountered with unprotected derivatives. For that reason **7** and **8** were re-protected in high yields with 4,4'-dimethoxytrityl (DMT) group to give the fully protected derivatives **9** and **10**, respectively. DMT group provided a hydrophobic tag which simplified work-up and purification of subsequent synthetic intermediates. Next, **9** and **10** were converted into *S*-(pyridyl-2-disulfanyl) derivative **11** using aqueous methylamine followed by the disulfide exchange reaction with 2,2'-dipyridyl disulfide. It is reported that the removal of 2'-*O*-acyl protection in ribofuranosyl derivatives similar to **9** and **10** proceeds with difficulty. Applicant found that 40% aqueous methylamine easily removed all acyl protecting groups from **9** and **10** and was the base of choice because, contrary to aqueous ammonia, it completely solubilised the fully protected substrates. *In situ* protection of SH as *S*-pyridyl-2-disulfanyl derivative was achieved using 2,2'-dipyridyl disulfide in DMF to afford **11** in 85% yield for these two steps.

In order to synthesize the free nucleoside, **13**, **11** was treated with dithiothreitol (DTT) in chloroform. When triethylamine was added to the reaction mixture the reaction was faster than in it's absence but at the same time **12** was converted into its *S*-TEA salt. Final deprotection of the DMT group of **12** was achieved with 1N HCl in methanol in the presence of DTT which quenched the released DMT-cation. In the absence of DTT, quantitative *S*-alkylation took place. Applicant is the first to report on the synthesis of the guanosine 3'-thio analog **13**. When unbuffered TBAF in THF was used to desilylate the

mixture of **4** and **5**, *S*-Ac protecting group was also removed leading to formation of the disulfide **14** (Scheme 2; **Figure 19**). Under these conditions the 3',4'-unsaturated derivative **15** remained intact and was separated from **14** by silica gel column chromatography. Products were invariably contaminated with TBAF. Attempted rechromatography of **15** led to its decomposition, though. Disulfide **14** was 5'-DMT protected to afford **16**.

The selective removal of the 3'-acetyl group of **16** (Scheme 2; **Figure 19**), followed by the introduction of 2'-*O*-*t*-butyldimethylsilyl (TBDMS) protection, then reduction of 3'-disulfide and 3'-phosphitylation would be the shortest way to prepare the desired 3'-thiophosphoramidite building block. Reactions of **16** with mild deacylating agents like basic ion exchangers in OH^- or CN^- form selectively removed 2'-*O*-acetyl protection, but at the same time nucleoside was strongly absorbed on the resin, resulting in low recoveries. Applicant used basic treatment followed by *S*-protection with *S*-pyridyl group, as used for the preparation of the *S*-pyridyl-2-disulfanyl derivative **11** from *S*-acylated **9** and **10**. In this manner **11** was obtained from the disulfide **16** in 67% yield.

The phosphoramidite synthesis is shown in Scheme 3 (**Figure 20**). Reaction of **11** with *N,N*-dimethylformamide dimethyl acetal yielded the desired *N*-protected derivative **18** in 23% yield. Unfortunately, this reagent also effected the cleavage of the *S*-pyridyl protection leading to formation of disulfide **17** in 33% yield. **18** was smoothly 2' protected with TBDMS group using *t*-butyldimethylsilyl trifluoromethanesulfonate (TBDMS-Tf). Alternatively, **11** was silylated with TBDMS-Cl to afford **20** and then *N*-protected using isobutyric anhydride (i-Bu_2O) in the presence of 4-dimethylaminopyridine (DMAP) yielding the fully protected **21**. In the absence of DMAP only starting material was recovered. On the other hand, reaction of **20** with isobutyryl chloride led to *N*-bis-acylation. Reduction of **21** with DTT afforded 3'-SH derivative **22**, which appeared as a mixture of two rotamers in ^1H NMR. Resonances of the major rotamer were in accordance with the ones reported by Sun *et al.* Phosphitylation of **22** under standard conditions afforded 3'-thiophosphoramidite **23**. Applicant has described an efficient synthesis of 3'-deoxy-3'-thio guanosine. Keeping all synthetic intermediates protected with lipophylic groups enabled their chromatographic purification and, consequently, a good recovery of the products.

Experimental Section

General. All reactions were carried out under a positive pressure of argon in anhydrous solvents. Commercially available reagents and anhydrous solvents were used without further purification. ^1H (400.075 MHz) and ^{31}P (161.947 MHz) NMR spectra

were recorded in $CDCl_3$, unless stated otherwise, and chemical shifts in ppm refer to TMS and H_3PO_4, respectively. Analytical thin-layer chromatography (TLC) was performed with Merck Art.5554 Kieselgel 60 F_{254} plates and flash column chromatography using Merck 0.040-0.063 mm silica gel 60. Mass spectra were obtained by fast atom bombardment method.

5'-*O*-*t*-Butyldiphenylsilyl-N^2-(dimethylaminomethylene)guanosine (2). To a stirred solution of N^2-(dimethylaminomethylene)guanosine (**1**) (5.5 g, 16.3 mmol) in pyridine (100 mL) *t*-butyldiphenylsilyl chloride (6.2 ml, 23.8 mmol) was added under argon. The reaction mixture was stirred at rt for 16 h, then quenched with methanol (20 ml) and evaporated to a syrup *in vacuo*. The residue was crystallized from ethanol-ether (9 g, 96%), mp, ^{1}H NMR (DMSO-d_6 + D_2O) d 8.46 (s, 1H, CH=N), 7.89 (s, 1H, H-8), 7.58-7.31 (m, 10H, Ph), 5.81 (d, $J_{1',2'}$=4.8, 1H, H-1'), 4.46 (app t, $J_{2',1'}$=4.8, 1H, H-2'), 4.23 (app t, $J_{3',2'}$=5.0, 1H, H-3'), 3.97 (m, 1H, H-4'), 3.84 (dd, $J_{5',4'}$=2.8, $J_{5',5''}$=12.0, 1H, H-5'), 3.74 (dd, $J_{5'',4'}$=4.4, $J_{5'',5'}$=12.0, 1H, H-5''), 3.05 (s, 3H, Me), 2.97 (s, 3H, Me), 0.94 (s, 9H, *t*-Bu), HRMS (FAB$^+$) calcd for $C_{29}H_{36}N_6O_5Si$ (MH^+): calc 577.2595, found 577.26095.

1-(2-*O*-Acetyl-5-*O*-*t*-Butyldiphenylsilyl-3-deoxy-3-bromo-b-D-xylofuranosyl)-N^2-(dimethylaminomethylene)guanosine (3). To a cooled (0 °C) solution of **2** (5.8 g, 10 mmol) and water (0.12 ml) in acetonitrile (130 ml) a-acetoxyisobutyryl bromide (5.56 ml, 38 mmol) was added and the mixture was stirred at rt for 3 h. The solution was poured into saturated aq. $NaHCO_3$ (100 mL) and extracted with CH_2Cl_2 (3 x 200 mL). The combined organic layers were dried (Na_2SO_4) and concentrated to give chromatographically pure white foam (6 g, 87%), ^{1}H NMR d 8.97 (br s, 1H, NH), 8.62 (s, 1H, CH=N), 7.82 (s, 1H, H-8), 7.73-7.31 (m, 10H, Ph), 6.09 (s, 1H, H-2'), 5.92 (d, $J_{1',2'}$=1.6, 1H, H-1'), 4.42 (m, 1H, H-4'), 4.36 (m, 1H, H-3'), 4.06 (dd, $J_{5',4'}$=5.6, $J_{5',5''}$=10.4, 1H, H-5'), 3.97 (dd, $J_{5'',4'}$=6.4, $J_{5'',5'}$=10.4, 1H, H-5''), 3.17 (s, 3H, *N*-Me), 3.07 (s, 3H, *N*-Me), 2.19 (s, 3H, *O*-Ac), 1.07 (s, 9H, *t*-Bu), HRMS (FAB$^+$) calcd for $C_{31}H_{37}BrN_6O_5Si$ (MH^+): calc 681.1856, found 681.1850.

1-(2-*O*-Acetyl-5-*O*-*t*-butyldiphenylsilyl-3-deoxy- b -D-*glycero*-pent-3-enofuranosyl-N^2-(dimethylaminomethylene)guanosine (4) and 2'-*O*-acetyl-5'-*O*-*t*-butyldiphenyl-silyl-3'-deoxy-3'-*S*-thioacetyl-N^2(dimethylaminomethylene)- guanosine (5). **3** (5.4 g, 7.9 mmol) was dissolved in dry DMF (50 ml) and potassium thioacetate (2.7 g, 23.6 mmol) was added to the solution. The reaction mixture was stirred at 60 °C for 16 h and then evaporated to a syrup under reduced pressure. The residue was partitioned between aq. $NaHCO_3$-brine 1:1 solution and dichloromethane, the organic layer was dried (Na_2SO_4), evaporated to dryness and chromatographed on the column of silicagel using 2-

10% gradient of methanol in dichloromethane **4** and **5** co-eluted yielding, after evaporation, a yellowish foam (4.8 g). ^{1}H NMR indicated a 3:7 ratio of **4** to **5**.

When potassium thiobenzoate was used instead of potassium thioacetate an inseparable mixture of **4** and **2'-*O*-acetyl-5'-*O*-*t*-butyldiphenylsilyl-3'-deoxy-3'-*S*-thiobenzoyl-N^2(dimethylaminomethylene)guanosine (6)** was obtained in a similar yield and ratio to the unsaturated derivative **4** as above.

2'-*O*-Acetyl-3'-deoxy-3'-*S*-thioacetyl-N^2(dimethylaminomethylene) guanosine (7). The above mixture of **4** an **5** (0.9 g) was dissolved in THF (15 ml) and acetic acid (0.37 ml, 6.5 mmol) was added followed by TBAF•3H_2O (0.82 g, 2.6 mmol). The reaction mixture was stirred at rt for 5 h, then diluted with dichloromethane, washed with water and 10% aq. $NaHCO_3$. Aqueous layers were back-washed with dichloromethane, organic layers were combined, dried (Na_2SO_4) and evaporated to dryness. Silica gel column chromatography using 2-10% gradient of methanol in dichloromethane afforded **7** as a yellowish foam (300 mg, ca 74%), ^{1}H NMR d 8.87 (br s, 1H, NH), 8.78 (s, 1H, CH=N), 7.73 (s, 1H, H-8), 5.80 (d, $J_{1',2'}$=2.0, 1H, H-1'), 5.76 (dd, $J_{2',1'}$=2.0, $J_{2',3'}$=6.4, 1H, H-2'), 4.94 (dd, $J_{3',2'}$=6.4, $J_{3',4'}$=9.6, 1H, H-3'), 4.22 (d, $J_{4',3'}$=9.6, 1H, H-4'), 4.04 (br s, 1H, 5'-OH), 3.99 (d, $J_{5',5''}$=12.0, 1H, H-5'), 3.71 (d, $J_{5'',5'}$=12.0, 1H, H-5''), 3.19 (s, 3H, *N*-Me), 3.04 (s, 3H, *N*-Me), 2.34 (s, 3H, *S*-Ac), 2.13 (s, 3H, *O*-Ac), HRMS (FAB$^+$) calcd for $C_{17}H_{22}N_6O_6S$ (MH^+): 439.1355, found 439.1405.

2'-*O*-Acetyl-3'-deoxy-3'-*S*-thiobenzoyl-N^2(dimethylaminomethylene) guanosine (8). Using the same procedure as above, **8** was synthesized from the mixture of **4** and **6** in ca 70% yield, ^{1}H NMR d 8.90 (br s, 1H, NH), 8.57 (brs, 1H, NH), 7.69 (s, 1H, H-8), 5.88 (m, 2H, H-1',H-2'), 5.30 (m, 1H, H-3'), 4.34 (d, $J_{4',3'}$=9.2, 1H, H-4'), 4.04 (d, $J_{5',5''}$=12.8, 1H, H5'), 3.80 (dd, $J_{5'',OH}$=9.6, $J_{5'',5''}$=12.8, 1H, H-5''), 3.69 (br s, 1H, 5'-OH), 3.25 (s, 3H, *N*-Me), 3.10 (s, 3H, *N*-Me), 2.16 (s, 3H, *O*-Ac), HRMS (FAB$^+$) calcd for $C_{17}H_{22}N_6O_6S$ (MH^+): 501.1556, found 501.1561.

2'-*O*-Acetyl-3'-deoxy-3'-*S*-thioacetyl-5'-*O*-*(4,4'-dimethoxytrityl)*-N^2(dimethylamino-methylene)guanosine (9). **7** (720 mg, 1.64 mmol) was dissolved in dry pyridine (15 ml) and DMT-Cl (1.1 g, 3.3 mmol) was added. The reaction mixture was stirred at rt for 4 h, qenched with methanol and evaporated to a syrup which was partitioned between 5% aq. $NaHCO_3$ and CH_2Cl_2. Organic layer was washed with brine, dried (Na_2SO_4) and evaporated to dryness *in vacuo*. The residue was purified by silica gel column chromatography using 1-5% gradient of methanol in dichloromethane to yield the product as a colorless foam (0.85 g, 70%), ^{1}H NMR d 8.69 (s, 1H, CH=N), 8.58 (br s, 1H, NH), 7.69 (s, 1H, H-8), 7.38-6.74 (m, 13H, H-8, aromatic), 6.06 (dd, $J_{2',3'}$=6.4, $J_{2',1'}$=1.2, 1H, H-2'), 5.82 (d, $J_{1',2'}$=1.2, 1H, H-1'), 4.73 (dd, $J_{3',4'}$=10.6, $J_{3',2'}$=6.4, 1H, H-3'), 4.21

(dq, $J_{4',3'}$=10.6, $J_{4',5'}$=3.0, $J_{4',5''}$=4.4, 1H, H-4'), 3.78 (s, 6H, 2xOMe), 3.36 (m, 2H, H-5', H-5"), 3.07 (s, 3H, *N*-Me), 3.05 (s, 3H, *N*-Me), 2.26 (s, 3H, *S*-Ac), 2.15 (s, 3H, O-Ac), HRMS (FAB$^+$) calcd for $C_{38}H_{40}N_6O_8S$ (MH^+): 741.2707, found 741.2692.

2'-*O*-Acetyl-3'-deoxy-3'-*S*-thiobenzoyl-5'-*O*-(4,4'-dimethoxytrityl)-N^2(dimethyl-aminomethylene)guanosine (10). Using similar procedure as described above, **8** was converted into **10** in 69% yield, ^{1}H NMR d 8.80 (s, 1H, CH=N), 8.65 (br s, 1H, NH), 7.70 (s, 1H, H-8), 7.88-6.66 (m, 19H, aromatic), 6.17 (d, $J_{2',3'}$=5.8, 1H, H-2'), 5.86 (d, $J_{1',2'}$=1.2, 1H, H-1'), 5.08 (dd, $J_{3',4'}$=10.4, $J_{3',2}$=5.8, 1H, H-3'), 4.31 (m, 1H, H-4'), 3.67 (s, 6H, 2xOMe), 3.45 (m, 2H, H-5', H-5"), 3.06 (s, 6H, 2X*N*-Me) 2.15 (s, 3H, *O*-Ac), HRMS (FAB$^+$) calcd for $C_{43}H_{42}N_6O_8S$ (MH^+): 803.2863, found 803.2855.

3'-Deoxy-3'-*S*-pyridylsulfanyl-5'-*O*-(4,4'-dimethoxytrityl)-guanosine (11). A. **9** (530 mg, 0.38 mmol) was dissolved in 40% aqueous methylamine (50 ml) and the mixture is kept at rt for 16 h. The solvent is removed in vacuo and the residual syrup dissolved in argon purged DMF (30 ml) containing 2,2'-dipyridyl disulfide (340 mg, 1.54 mmol). The reaction mixture is heated at 60 °C for 10 h and then evapprated to a syrup *in vacuo*. Column chromatography on silica gel using 1-12% gradient of methanol in dichloromethane afforded **11** as a colorless solid (460 mg, 85%), ^{1}H NMR d 10.64 (br s, 1H, NH), 8.39 (m, 1H, Pyr), 7.83 (s, 1H, H-8), 7.73-6.72 (m, 16H, aromatic), 6.50 (d, $J_{OH,2'}$=4.80, 1H, OH-2'), 6.45 (br s, 2H, NH_2), 5.81 (d, $J_{1',2'}$=2.4, 1H, H-1'), 4.83 (m, 1H, H-2'), 4.34 (m, 1H, H-4'), 4.09 (dd, $J_{3'2'}$=6.00, $J_{3',4'}$=7.8, 1H, H-3'), 3.70 (s, 6H, 2XOMe), 3.11 (dd, $J_{5',5''}$=11.2, $J_{5'',4'}$=4.8, 1H, H-5"), HRMS (FAB$^+$) calcd for $C_{36}H_{34}N_6O_6S_2$ (MH^+): 711.2060, found 711.2076.

B. Using the same procedure as above, but starting from *S*-benzoyl derivative **10**, **11** was prepared in 80% yield.

C. Starting from **16** (830 mg, 1.12 mmol) and using the above conditions **11** (570 mg, 67%) was obtained .

3'-Deoxy-3'-thio-5'-*O*-(4,4'-dimethoxytrityl)-guanosine (12). To the solution of **11** (240 mg, 0.34 mmol) in chloroform (14 ml) dithiothreitol (DTT) (125 mg, 0.81 mmol) was added and the reaction mixture was stirred at rt for 3 h. It was then evaporated to a syrup *in vacuo*, and the product was precipitated by addition of peroxide-free ether, precipitate was filtered off, washed with ether and dried (230 mg of the crude material), ^{1}H NMR (DMSO-d_6) d 10.63 (br s, 1H, NH), 7.86 (s, 1H, H-8), 7.32-6.80 (m, 13H, aromatic), 6.49 (br s, 2H, NH_2), 5.81 (s, 1H, H-1'), 4.43 (d, $J_{2',3'}$=4.8, 1H, H-2'), 3.93 (m, 1H, H-4'), 3.79 (dd, $J_{3'2'}$=4.8, $J_{3',4'}$=9.6, 1H, H-3'), 3.71 (s, 6H, 2XOMe), 3.16 (dd, $J_{5'',5'}$=10.4, $J_{5'',4'}$=4.8, 1H, H-5").

3'-Deoxy-3'-thio-guanosine (13). The mixture of the crude **12** (230 mg, 0.33 mmol) and DTT (150 mg) was dissolved in 1 N methanolic HCl (12 ml) and the reaction mixture was kept at rt for 3 h. It was then concentrated *in vacuo* and the residue coevaporated with toluene two times. Addition of ethyl acetate afforded precipitate which was filtered off, washed well with ethyl acetate and dried to afford **13** (90 mg, 79%). The product was reprecipitated from water, ^{1}H NMR (CD_3OD) d 8.10 (s, 1H, H-8), 5.91 (s, 1H, H-1'), 4.37 (d, $J_{2',3'}$=5.2, 1H, H-2'), 3.97 (m, 2H, H-4', H-5'), 3.82 (dd, $J_{5'',5'}$=13.0, $J_{5'',4'}$=3.4, 1H, H-5"), 3.64 (dd, $J_{3',2'}$=5.2, $J_{3',4'}$=9.6, 1H, H-3'), HRMS (FAB$^+$) calcd for $C_{10}H_{13}N_5O_4S$ (MH$^+$): 300.0767, found 300.0767.

Bis (2-*O*-acetyl-N^2-(dimethylaminomethylene)guanosin-3-yl)disulfide (14) and 1-(2-*O*-acetyl-3-deoxy- b -D-*glycero*-pent-3-enofuranosyl)-N^2-(dimethyl-aminomethylene) guanosine (15). The mixture of **4** and **5** (4.8 g) was dissolved in THF (100 mL) and 1M TBAF in THF (10 mL) was added. The reaction mixture was stirred for 3 h at rt and then evaporated to a syrup *in vacuo*. Silica gel column chromatography using 2-10% gradient of methanol in dichloromethane yielded the faster eluting **15** (1 g, 35% for two steps from **3**, colorless foam), ^{1}H NMR d 8.96 (br s, 1H, NH), 8.57 (s, 1H, CH=N), 7.65 (s, 1H, H-8), 6.41 (s, 1H, H-2'), 6.04 (s, 1H, H-1'), 5.42 (m, 1H, H-3'), 4.32 (m, 2H, H-5',H-5"), 3.19 (s, 3H, *N*-Me), 3.06 (s, 3H, *N*-Me), 2.11 (s, 3H, Ac). The slower eluting **14** was obtained as a yellowish solid (0.9 g, 29% for two steps), ^{1}H NMR (DMSO-d_6) d 11.34 (br s, 1H, NH), 8.53 (s, 1H, CH=N), 8.00 (s, 1H, H-8), 5.97 (d, $J_{1',2'}$=2.4, 1H, H-1'), 5.89 (dd, $J_{2',1'}$=2.4, $J_{2',3'}$=6.0, 1H, H-2'), 5.23 (t, $J_{OH,5'}$=5.6, 1H, 5'-OH), 4.11 (m, 1H, H-4'), 4.02 (dd, $J_{3',2'}$=6.0, $J_{3',4'}$=8.4, 1H, H-3'), 3.78 (dm, $J_{5',5''}$=12.0, 1H, H-5'), 3.60 (dm, $J_{5'',5'}$=12.0, 1H, H-5"), 3.10 (s, 3H, *N*-Me), 3.00 (s, 3H, *N*-Me), 2.06 (s, 3H, *O*-Ac), HRMS (FAB$^+$) calcd for $C_{30}H_{38}N_{12}O_{10}S_2$ (MH$^+$): 791.2354, found 791.2355.

Bis (2-*O*-acetyl-5-*O*-(4,4'dimethoxytrityl)-N^2-(dimethylaminomethylene) guanosin-3-yl) disulfide (16). To the solution of **14** (400 mg, 0.5 mmol) in dry pyridine (10 ml) DMT-Cl (508 mg, 1.5 mmol) was added and the mixture was stirred 4 h at rt. Methanol (10 ml) was added and the solution evaporated to dryness. The residue is partitioned between saturated $NaHCO_3$ and dichloromethane, organic layer washed with brine, dried (Na_2SO_4) and evaporated to a syrup. Silica gel column chromatography using 2-10% gradient of methanol in dichloromethane yielded product as a yellowish foam (620 mg, 71% yield), ^{1}H NMR d 8.72 (br s, 1H, NH), 8.01 (s, 1H, CH=N), 7.48-7.21 (m, 14H, H-8, aromatic), 6.25 (d, $J_{2',3'}$=4.8, 1H, H-2'), 5.78 (s, 1H, H-1'), 4.00 (m, 2H, H-3', H-4'), 3.78 (s, 6H, 2xOMe), 3.50 (br s, 2H, H-5',H-5"), 3.14 (s, 3H, *N*-Me), 3.13 (s, 3H, *N*-Me), 1.82 (s, 3H, *O*-Ac), HRMS (FAB$^+$) calcd for C72H74N12O14S2 (MH+): 1395.4967, found 1395.4943.

Bis (5-*O*-(4,4'dimethoxytrityl)-N^2-(dimethylaminomethylene) guanosin-3-yl)-disulfide (17). A. 16 (60 mg, 0.04 mmol) is dissolved in dry methanol and ion exchange resin AG 1X8 (OH^-) (1 g) is added. The mixture was stirred at 55 °C for 16 h, the resin was filtered off and washed well with hot methanol. The filtrate was evaporated to dryness *in vacuo* yielding pure **17** as a colorless solid (16 mg, 28%), ^{1}H NMR (DMSO-d_6) d 11.34 (br s, 1H, NH), 8.48 (s, 1H, CH=N), 7.92 (s, 1H, H-8), 7.31-6.73 (m, 13H, aromatic), 6.27 (d, $J_{OH,2'}$=5.2, 1H, 2'-OH), 5.88 (d, $J_{1',2'}$=1.2, 1H, H-1'), 4.60 (m,1H, H-2'), 4.16 (m, 1H, H-4'), 4.08 (m, 1H, H-3'), 3.65 (s, 6H, 2XOMe), 3.65 (m, 2H, H-5', H-5"), 3.02 (s, 3H, *N*-Me), 2.97 (s, 3H, *N*-Me), HRMS (FAB^+) calcd for $C_{68}H_{70}N_{12}O_{12}S_2$ (MH^+): 1311.4756, found 1311.4746.

B. Using Amberlyst A-26 (CN^-) under the the above reaction conditions, **17** was obtained from **16** in 21% yield.

3'-Deoxy-3'-*S*-pyridylsulfanyl-5'-*O*-(4,4'-dimethoxytrityl)-N^2-(dimethylamino-methylene)guanosine (18) and 17. To the solution of **11** (400 mg, 0.56 mmol) in dry pyridine (5 ml), *N,N*-dimethylformamide dimethyl acetal (1.2 ml, 9 mmol) was added and the reaction mixture was stirred at rt for 16 h. Solvents were removed in vacuo and the residue chromatographed on the column of silica gel using 1-50% gradient of methanol in dichloromethane. Fractions containing the faster running material were combined and concentrated *in vacuo* to give **18** (110 mg, 23%), ^{1}H NMR d 8.73 (br s, 1H, NH), 8.53 (s, 1H, CH=N), 8.49 (m, 1H, pyridine), 7.71 (s, 1H, H-8), 7.62 (m, 1H, pyridine), 7.44-6.79 (m, 15H, aromatic), 6.09 (s, 1H, H-1'), 4.55 (d, $J_{2',3'}$=4.8, 1H, H-2'), 4.23 (dq, $J_{4',3'}$=10.5, $J_{4',5'}$=2.8, $J_{4',5"}$=3.4, 1H, H-4'), 4.14 (dd, $J_{3'2'}$=4.8, $J_{3',4'}$=10.5, 1H, H-3'), 3.78 (s, 6H, 2XOMe), 3.57 (dd, $J_{5',5"}$=10.6. $J_{5',4'}$=2.8. 1H, H-5'), 3.41 (dd, $J_{5',5"}$=10.6, $J_{5",4'}$=3.4, 1H, H-5"), 3.08 (s, 3H, *N*-CH_3), 3.05 (s, 3H, *N*-CH_3). Fractions containing the slower running compound were collected and evaporated to dryness *in vacuo* to give **17** as a colorless foam (120 mg, 33%), ^{1}H NMR identical to that of **17** obtained obtained using the above procedures.

2'-*O*-*t*-Butyldimethylsilyl-3'-deoxy-3'-*S*-pyridylsulfanyl-5'-*O*-(4,4'-dimethoxytrityl)--N^2-(dimethylamino-methylene) guanosine (19). 18 (110 mg, 0.14 mmol) was dissolved in dry pyridine (1 ml) and TBDMS-Tf (0.103 ml, 0.45 mmol) was added to the solution. The reaction mixture was stirred at rt for 5 h, then qunched with methanol and evaporated to a syrup *in vacuo*. The residue was dissoved in dichloromethane, washed with 5% aqueous $NaHCO_3$, then brine and the organic layer was dried (Na_2SO_4) and concentrated to the syrup. Column chromatography on silica gel using 1-10% gradient of methanol in ethyl acetate afforded **19** as a colorless solid (90 mg, 71%), ^{1}H NMR d 8.69 (br s, 1H, NH), 8.50 (s, 1H, CH=N), 8.37 (m, 1H, pyridine), 7.81

(s, 1H, H-8), 7.50-6.74 (m, 16H, aromatic), 5.98 (d, $J_{1',2'}$=2.4, 1H, H-1'), 4.75 (dd, $J_{2',3'}$=5.0, $J_{2',1'}$=2.4, 1H, H-2'), 4.50 (m,1H, H-4'), 3.99 (dd, $J_{3'2'}$=5.0, $J_{3',4'}$=8.4, 1H, H-3'), 3.76 (s, 6H, 2XOCH$_3$), 3.62 (dd, $J_{5',5''}$=10.9. $J_{5',4'}$=2.2. 1H, H-5'), 3.38 (dd, $J_{5',5''}$=10.9, $J_{5'',4'}$=4.4, 1H, H-5''), 3.06 (s, 3H, *N*CH$_3$), 3.04 (s, 3H, *N*CH$_3$), 0.93 (s, 9H, *t*-Bu), 0.17 (s, 3H, Me), 0.10 (s, 3H, Me), HRMS (FAB$^+$) calcd for $C_{45}H_{53}N_7O_6S_2Si$ (MH$^+$) 880.3346, found 880.3357.

2'-*O*-*t*-Butyldimethylsilyl-3'-deoxy-3'-*S*-pyridylsulfanyl-5'-*O*-(4,4'-dimethoxytrityl) guanosine (20). 3'-Deoxy-3'-*S*-pyridylsulfanyl-5'-*O*-(4,4'-dimethoxytrityl)guanosine **11** (410 mg, 0.58 mmol) was dissolved in dry pyridine (36 ml) and imidazole (2.36 g, 35 mmol) and TBDMS-Cl (4.29 g, 28 mmol) were added. The reaction was stirred at rt 16 h, then evaporated to a syrup in vacuo. The residue was partitioned between dichloromethane and saturated aq. NaHCO$_3$, organic layer washed with water, dried (Na$_2$SO$_4$) and concentrated to a syrup. Column cgromatography on silica gel using 1-10% gradient of methanol in dichloromethane afforded the product as a white foam (430 mg, 85%), ^{1}H NMR (DMSO-d$_6$) d 11.99 (br s, 1H, NH), 8.39 (m, 1H, Pyr), 7.84 (s, 1H, H-8), 7.71 (m, 1H, Pyr), 7.62-6.72 (m, 15H, aromatic) 6.41 (br s, 2H, NH$_2$), 5.80 (d, $J_{1',2'}$=4.4, 1H, H-1'), 5.04 (app t, $J_{2',3'}$=4.4, 1H, H-2'), 4.39 (m, 1H, H-4'), 4.01 (app t, $J_{3',4'}$=6.4, 1H, H-3'), 3.69 (s, 6H, 2XOMe), 3.13 (dd, $J_{5'',5'}$=11.0, $J_{5'',4'}$=4.6, 1H, H-5''), 0.82 (s, 9H, *t*-Bu), 0.08 (s, 3H, Me), 0.06 (s, 3H, Me), HRMS (FAB$^+$) calcd for $C_{42}H_{48}N_6O_6S_2Si$ (MH$^+$) 825.2924, found 825.2977.

2'-*O*-*t*-Butyldimethylsilyl-3'-deoxy-3'-*S*-pyridylsulfanyl-5'-*O*-(4,4'-dimethoxytrityl)-*N*^{2}-isobutyrylguanosine (21). To the solution of **20** (310 mg, 0.38 mmol) in dry pyridine (5 ml) isobutyric anhydride (0.19 ml, 1.14 mmol) and DMAP (46 mg, 0.38 mm) were added and the mixture was stirred at rt 16 h. It was then stirred at 50 °C for 5 h, quenched with methanol (2 ml) and evaporated to a syrup *in vacuo*. The residue was partitioned between dichloromethane and 5% aqueous NaHCO$_3$, the organic layer was washed with brine, dried (Na$_2$SO$_4$) and evaporated to a syrup. Column chromatography on silica gel using 1-5% gradient of methanol in CH$_2$Cl$_2$ afforded product as a colorless foam (320 mg, 95%), ^{1}H NMR d 11.94 (br s, 1H, NH), 8.36 (m, 1H, Pyr), 7.85 (m, 1H, Pyr), 7.80 (s, 1H, H-8), 7.58-6.71 (m, 16H, NH, aromatic), 5.83 (d, $J_{1',2'}$=5.2, 1H, H-1'), 5.22 (app t, $J_{1',2'}$=5.2, 1H, H-2'), 4.50 (m, 1H, H-4'), 4.27 (app t, $J_{3',4'}$=6.4, 1H, H-3'), 3.76 (s, 3H, OMe), 3.75 (s, 3H, OMe), 3.56 (dd, $J_{5',5''}$=11.0, $J_{5',4'}$=1.8, 1H, H5'), 2.98 (dd, $J_{5'',5'}$=11.0, $J_{5'',4'}$=3.0, 1H, H-5''), 1.69 (m, 1H, *CH*Me$_2$), 0.94 (d, J=7.2, 3H, CH$_3$), 0.76 (d, J=7.2, 3H, CH$_3$), 0.88 (s, 9H, *t*-Bu), 0.11 (s, 3H, Me), 0.06 (s, 3H, Me), HRMS (FAB$^+$) calcd for $C_{46}H_{54}N_6O_7S_2Si$ (MH$^+$) 895.3343, found 895.3380.

2'-*O*-*t*-Butyldimethylsilyl-3'-deoxy-3'-thio-5'-*O*-(4,4'-dimethoxytrityl)-N^2-isobutyrylguanosine (22). To the solution of **21** (340 mg, 0.38 mmol) in chloroform (20 ml) TEA (0.4 ml) and dithiotreitol DTT (140 mg, 0.91 mmol) were added and the reaction mixture was stirred for 1 h at rt. The reaction miture was washed with saturated aqueous $NaHCO_3$, water, dried (Na_2SO_4) and concentrated to a syrup. Silica gel column chromatography using 0.5-2% gradient of methanol in CH_2Cl_2 afforded **22** (270 mg, 90%), ^1H NMR for the major rotamer: d 11.92 (br s, 1H, NH), 7.93 (s, 1H, H-8), 7.63-6.80 (m, 16H, NH, aromatic), 5.83 (d, $J_{1',2'}$=2.8, 1H, H-1'), 4.74 (dd, $J_{2',1'}$=2.8, $J_{2',3'}$=5.4, 1H, H-2'), 4.13 (dd, $J_{4',3'}$=7.6, $J_{4',5'}$=1.2, 1H, H-4'), 3.78 (s, 3H, OMe), 3.73 (s, 3H, OMe), 3.63 (dd, $J_{5',5''}$=11.0, $J_{5',4'}$=1.2, 1H, H5'), 3.27 (dd, $J_{5'',5'}$=11.0, $J_{5'',4'}$=3.0, 1H, H-5''), 1.63 (d, $J_{SH,3'}$=8.4, 1H, SH), 2.08 (m, 1H, *CH*Me_2), 1.09 (d, J=6.8, 3H, CH_3), 0.98 (d, J=6.8, 3H, CH_3), 0.91 (s, 9H, *t*-Bu), 0.14 (s, 3H, Me), 0.08 (s, 3H, Me), HRMS (FAB^+) calcd for $C_{41}H_{51}N_5O_7SSi$ (MH^+) 786.3357, found 786.3354.

2'-*O*-*t*-Butyldimethylsilyl-3'-deoxy-3'-thio-5'-*O*-(4,4'-dimethoxytrityl)-N^2-isobutyrylguanosine 3'-*S*-(2-cyanoethyl *N,N*-diisopropylphoramidite (23). Phosphitylation of **22** as described by Sun *et al.* afforded product which was purified by flash chromatography using 0.5% ethanol in CH_2Cl_2 containing 1% TEA. Final product was obtained as a white powder by precipitation from toluene-pentane at 0 °C (76% yield), ^{31}P NMR d 163.5 (s), 159.6 (s), HRMS (FAB^+) calcd for $C_{50}H_{68}N_7O_8PSSi$ (MH^+) 986.4435, found 986.4406.

Example 13: Synthesis of 5'- thiophosphate nucleoside phosphoramidite and preparation of solid support

Referring to **Figure** 21, Applicant shows a scheme for synthesis of 5'-deoxy-5'-thionucleoside phosphoramidites and succinates. For example Lehmann *et al.*, (*NAR* 1989, 17, 2379; incorporated by reference herein) describes the preparation of the more base-stable sarcosyl modified solid support.

Matulic-Adamic. *et al.* in *Nucleosides & Nucleosides* 1997, 16, 1933, describes the incorporation of 5'-thio modification into oligonucleotides. Applicant additionally describes the a method where, the cleavage of the 5'-protecting group on the solid support in order to elongate the chain is accomplished by using, instead of AgNO3 in CH3CN, 0.1M 1,8-diazabicyclo[5.4.0]undec-7-ene (DBU) in CH3CN or 20% piperidine in CH3CN.

Note that 5'S-DMT protection is cleaved with iodine (Henningfeld *et al. JACS* 1996, 118, 11701) thus complicating the oligo synthesis, while S-Fm is reported to be resistant to 0.1 M iodine in DMF.

Oligonucleotides were synthesized with 5'-thiophosphate linkage and tested *in vitro* in a standard RNase H cleavage assay described in McSwiggen, US Patent No. 5,525,468; incorporated by reference herein.

Example 14: Synthesis of 5'-*O*-dimethoxytrityl-3'-deoxy-3'-thio-3'-*S*-(2-Cyanoethyl-N,N-Diisopropylphosphoramidite-2'-*O*-methyl uridine **(6) (Figure 22)**

5'-O-tert-butyldiphenylsilyl-2'-O-methyl uridine **(1)**: To a solution of 2'-*O*-methyl uridine stirring at 0 C under positive pressure argon in anhydrous pyridine was added *tert*-butyldiphenylsilyl chloride (1.2 eq.) The reaction mixture was allowed to warm to rt and was maintained at rt for 18 hours at which time ethanol was added, pyridine removed in vacuo, and the reaction residue partitioned between dichloromethane and sat. aq. sodium bicarbonate. The organic layer was then dried over sodium sulfate. Flash chromatography using an ethyl acetate/hexanes gradient gave (1) as a white foam.

5'-O-tert-butyldiphenylsilyl-2'-O-methyl-2,3'-anhydro uridine **(2)**: To a solution of **(1)** and DEAD (3.5 eq.) stirring at 0 C under argon in anhydrous THF was added triphenylphosphine (3.5 eq.). The reaction mixture was warmed to rt and stirred at rt under argon for 18 hours, after which THF was removed *in vacuo*. The crude reaction residue was partitioned between dichloromethane and sat. aq. sodium bicarbonate, the organics dried over sodium sulfate preceding flash chromatography. An ethyl acetate/hexanes gradient afforded (2) as an off white foam.

5'-O-tert-butyldiphenylsilyl-3'-S-acetyl-2'-O-methyl uridine **(3)**: Compound **(2)** was treated with thiolacetic acid in dioxane at 100 C for 18 hours while stirring in a stainless steel bomb. The reaction mixture was evaporated *in vacuo* then purified by flash silica gel chromatography to give **(3)** as a light yellow foam.

5'-O-dimethoxytrityl-3'-S-acetyl-2'-O-methyl uridine **(4)**: To a solution of (3) stirring at rt under positive pressure argon was added 1M TBAF in THF buffered with acetic acid. The resulting clear, light yellow solution was stirred at rt for one hour, then THF removed *in vacuo*. Crude (4) was flash silica purified using an ethanol/dichloromethane gradient. The purified product was then co-evaporated with anhydrous pyridine, then dissolved in anhydrous pyridine. Dimethoxytrityl chloride was added to the reaction at rt and the resulting clear, reddish solution stirred at rt for 18 hours. Pyridine was removed in vacuo after quenching with ethanol, and the resulting crude foam partitioned between dichloromethane and sat. aq. sodium bicarbonate and the organics dried over sodium sulfate. Flash chromatography using an ethyl acetate/hexanes gradient furnished pure (4).

5'-O-dimethoxytrityl-3'-deoxy-3'-thio-2'-O-methyl uridine **(5)**: Compound (4) was dissolved in 40% aq. methylamine in the presence of DTT. The reaction mixture was stirred at rt for one hour then evaporated *in vacuo*. Flash chromatography using an ethyl acetate/hexanes gradient gave (5) as an off white foam.

5'-O-dimethoxytrityl-3'-deoxy-3'-thio-3'-S-(2-Cyanoethyl-N,N-Diisopropylphosphoramidite-2'-O-methyl uridine **(6)**: To a cooled (0 °C) solution of (5) and *N,N*-diisopropylethylamine in dry CH_2Cl_2 was added 2-cyanoethyl *N,N*-diisopropylchlorophosphoramidite dropwise via syringe. The mixture was stirred at room temperature until all starting material was consumed (5 hr.) The reaction mixture was quenched with anhydrous ethanol and diluted with hexanes. Flash chromatography using an ethyl acetate/hexanes gradient provided pure (6).

Diagnostic uses

Nucleic acid molecules of this invention may be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of specific RNAs in a cell. The close relationship between for example ribozyme activity and the structure of the target RNA allows the detection of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple ribozymes described in this invention, one may map nucleotide changes which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with ribozymes may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic targets may be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combinational therapies (e.g., multiple nucleic acid molecules targeted to different genes, nucleic acid molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations of nucleic acid molecules and/or other chemical or biological molecules). Other *in vitro* uses of nucleic acid molecules of this invention are well known in the art, and include detection of the presence of RNAs related to various conditions. Such RNA is detected by determining the presence of a cleavage product after treatment with for example, an enzymatic nucleic acid molecule using standard methodology.

In a specific example, ribozymes which can cleave only wild-type or mutant forms of the target RNA are used for the assay. The first ribozyme is used to identify wild-type RNA present in the sample and the second ribozyme will be used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant

RNA will be cleaved by both ribozymes to demonstrate the relative ribozyme efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates will also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus each analysis will require two ribozymes, two substrates and one unknown sample which will be combined into six reactions. The presence of cleavage products will be determined using an RNAse protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of a phenotype is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels will be adequate and will decrease the cost of the initial diagnosis. Higher mutant form to wild-type ratios will be correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

Additional Uses

Potential usefulness of sequence-specific enzymatic nucleic acid molecules of the instant invention might have many of the same applications for the study of RNA that DNA restriction endonucleases have for the study of DNA (Nathans *et al.*, 1975 *Ann. Rev. Biochem.* 44:273). For example, the pattern of restriction fragments could be used to establish sequence relationships between two related RNAs, and large RNAs could be specifically cleaved to fragments of a size more useful for study. The ability to engineer sequence specificity of the ribozyme is ideal for cleavage of RNAs of unknown sequence.

Other embodiments are within the following claims.

TABLE I

Characteristics of naturally occurring ribozymes

Group I Introns

- Size: ~150 to >1000 nucleotides.
- Requires a U in the target sequence immediately 5' of the cleavage site.
- Binds 4-6 nucleotides at the 5'-side of the cleavage site.
- Reaction mechanism: attack by the 3'-OH of guanosine to generate cleavage products with 3'-OH and 5'-guanosine.
- Additional protein cofactors required in some cases to help folding and maintainance of the active structure.
- Over 300 known members of this class. Found as an intervening sequence in *Tetrahymena thermophila* rRNA, fungal mitochondria, chloroplasts, phage T4, blue-green algae, and others.
- Major structural features largely established through phylogenetic comparisons, mutagenesis, and biochemical studies [1,2].
- Complete kinetic framework established for one ribozyme [3,4,5,6].
- Studies of ribozyme folding and substrate docking underway [7,8,9].

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- Chemical modification investigation of important residues well established [10,11].
- The small (4-6 nt) binding site may make this ribozyme too non-specific for targeted RNA cleavage, however, the Tetrahymena group I intron has been used to repair a "defective" β-galactosidase message by the ligation of new β-galactosidase sequences onto the defective message [12].

RNAse P RNA (M1 RNA)

- Size: ~290 to 400 nucleotides.
- RNA portion of a ubiquitous ribonucleoprotein enzyme.
- Cleaves tRNA precursors to form mature tRNA [13].
- Reaction mechanism: possible attack by M^{2+}-OH to generate cleavage products with 3'-OH and 5'-phosphate.
- RNAse P is found throughout the prokaryotes and eukaryotes. The RNA subunit has been sequenced from bacteria, yeast, rodents, and primates.
- Recruitment of endogenous RNAse P for therapeutic applications is possible through hybridization of an External Guide Sequence (EGS) to the target RNA [14,15]
- Important phosphate and 2' OH contacts recently identified [16,17]

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Group II Introns

- Size: >1000 nucleotides.
- Trans cleavage of target RNAs recently demonstrated [18,19].
- Sequence requirements not fully determined.
- Reaction mechanism: 2'-OH of an internal adenosine generates cleavage products with 3'-OH and a "lariat" RNA containing a 3'-5' and a 2'-5' branch point.
- Only natural ribozyme with demonstrated participation in DNA cleavage [20,21] in addition to RNA cleavage and ligation.
- Major structural features largely established through phylogenetic comparisons [22].
- Important 2' OH contacts beginning to be identified [23]
- Kinetic framework under development [24]

Neurospora VS RNA

- Size: ~144 nucleotides.
- TRANS CLEAVAGE OF HAIRPIN TARGET RNAS RECENTLY DEMONSTRATED [25].
- Sequence requirements not fully determined.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.

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- Binding sites and structural requirements not fully determined.
- Only 1 known member of this class. Found in Neurospora VS RNA.

Hammerhead Ribozyme

(see text for references)

- Size: ~13 to 40 nucleotides.
- Requires the target sequence UH immediately 5' of the cleavage site.
- Binds a variable number nucleotides on both sides of the cleavage site.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- 14 known members of this class. Found in a number of plant pathogens (virusoids) that use RNA as the infectious agent.
- Essential structural features largely defined, including 2 crystal structures [26,27]
- Minimal ligation activity demonstrated (for engineering through *in vitro* selection) [28]
- Complete kinetic framework established for two or more ribozymes [29].
- Chemical modification investigation of important residues well established [30].

Hairpin Ribozyme

- Size: ~50 nucleotides.
- Requires the target sequence GUC immediately 3' of the cleavage site.
- Binds 4-6 nucleotides at the 5'-side of the cleavage site and a variable number to the 3'-side of the cleavage site.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.

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- 3 known members of this class. Found in three plant pathogen (satellite RNAs of the tobacco ringspot virus, arabis mosaic virus and chicory yellow mottle virus) which uses RNA as the infectious agent.
- Essential structural features largely defined [31,32,33,34]
- Ligation activity (in addition to cleavage activity) makes ribozyme amenable to engineering through *in vitro* selection [35]
- Complete kinetic framework established for one ribozyme [36].
- Chemical modification investigation of important residues begun [37,38].

Hepatitis Delta Virus (HDV) Ribozyme

- Size: ~60 nucleotides.
- Trans cleavage of target RNAs demonstrated [39].
- Binding sites and structural requirements not fully determined, although no sequences 5' of cleavage site are required. Folded ribozyme contains a pseudoknot structure [40].

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- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- Only 2 known members of this class. Found in human HDV.
- Circular form of HDV is active and shows increased nuclease stability [41]

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Table II: 2.5 µmol RNA Synthesis Cycle

Reagent	Equivalents	Amount	Wait Time*
Phosphoramidites	6.5	163 µL	2.5
S-Ethyl Tetrazole	23.8	238 µL	2.5
Acetic Anhydride	100	233 µL	5 sec
N-Methyl Imidazole	186	233 µL	5 sec
TCA·	83.2	1.73 mL	21 sec
Iodine	8.0	1.18 mL	45 sec
Acetonitrile	NA	6.67 mL	NA

Table IIIA. Antisense Sequences and Corresponding in vitro Data

Seq. I.D. No.	Target	Cell Line	Sequence	Inhibition
2717	c-raf	PC-3	$u_sc_sc_scgc[C_sT_sG_sT_sG_sA_sC_s]augc_sa_su_sT$	70-80%
2718	Estrogen Receptor (ER)	MCF-7	$a_sg_sc_sauccaa[C_sA_sA_sG_sG_sC_sA_s]cugacc_sa_su_sc$	53%
2719	Estrogen Receptor (ER)	MCF-7	$c_sa_sg_scaucca[A_sC_sA_sA_sG_sG_sC_s]acugac_sc_sa_su$	48%
2720	Estrogen Receptor (ER)	MCF-7	$c_su_sg_sccaggu[T_sG_sG_sT_sC_sA_sG_s]uaagcc_sc_sa_su$	60%
2721	Estrogen Receptor (ER)	MCF-7	$u_su_su_scccugg[T_sT_sC_sC_sT_sG_sT_s]ccaaga_sg_sc_sa$	59%
2722	Estrogen Receptor (ER)	MCF-7	$c_sc_sa_sgcauc[T_sC_sC_sA_sG_sC_sA_s]gcagg_su_sc_sa$	61%
2723	Estrogen Receptor (ER)	MCF-7	$c_sg_su_sccagc[A_sT_sC_sT_sC_sC_sA_s]gcagc_sa_sg_sg$	64%

Table IIIB. Ribozyme sequences and Corresponding *in vitro* Data

Seq. I.D. No.	Target	Cell Line	Sequence	Inhibition
2724	Estrogen Receptor (ER)	MCF-7	[$A_sT_sA_sG_sA_sT_sT_sT_s$] cUGAuGaggccgaaaggccGaa Aggcacac B	50%
2725	Estrogen Receptor (ER)	MCF-7	$g_sg_su_s$cagu cUGAuGaggccguuaggccGaa Agccc[$A_sT_sC_sA_sT_sC_sG$] B	see figure 4
2726	Control	MCF-7	$g_su_sc_s$ggcc cUuAuGaggccguuaggccGau Acagu[$T_sA_sG_sCsC_sT_sA$] B	See figure 4

Lower case = 2'OMe

U = 2'-C-Allyl-U

G,A= ribo G,A

s = phosphorothioate linkages

B = inverted abasic

[G,A,C,T]= DNA

Table IV. Hammerhead Ribozyme and Target SequencesFor Estrogen Receptor

Pos	RZ	Seq. ID. No.	Substrate	Seq. ID. No.
22	UUGGCUUA CUGAUGAG X CGAA ACAUCACU	1	AGTGATGT T TAAGCCAA	1246
23	AUUGGCUU CUGAUGAG X CGAA AACAUCAC	2	GTGATGTT T AAGCCAAT	1247
24	CAUUGGCU CUGAUGAG X CGAA AAACAUCA	3	TGATGTTT A AGCCAATG	1248
34	CUUGCCCU CUGAUGAG X CGAA ACAUUGGC	4	GCCAATGT C AGGGCAAG	1249
51	CGGCCAGG CUGAUGAG X CGAA ACUGUUGC	5	GCAACAGT C CCTGGCCG	1250
61	UGCUGGAG CUGAUGAG X CGAA ACGGCCAG	6	CTGGCCGT C CTCCAGCA	1251
64	AGGUGCUG CUGAUGAG X CGAA AGGACGGC	7	GCCGTCCT C CAGCACCT	1252
73	GCAUUACA CUGAUGAG X CGAA AGGUGCUG	8	CAGCACCT T TGTAATGC	1253
74	UGCAUUAC CUGAUGAG X CGAA AAGGUGCU	9	AGCACCTT T GTAATGCA	1254
77	AUAUGCAU CUGAUGAG X CGAA ACAAAGGU	10	ACCTTTGT A ATGCATAT	1255
84	CGAGCUCA CUGAUGAG X CGAA AUGCAUUA	11	TAATGCAT A TGAGCTCG	1256
91	GGUCUCCC CUGAUGAG X CGAA AGCUCAUA	12	TATGAGCT C GGGAGACC	1257
103	ACUUUAAG CUGAUGAG X CGAA ACUGGUCU	13	AGACCAGT A CTTAAAGT	1258
106	CCAACUUU CUGAUGAG X CGAA AGUACUGG	14	CCAGTACT T AAAGTTGG	1259
107	UCCAACUU CUGAUGAG X CGAA AAGUACUG	15	CAGTACTT A AAGTTGGA	1260
112	GGGCCUCC CUGAUGAG X CGAA ACUUUAAG	16	CTTAAAGT T GGAGGCCC	1261
148	CCAGGACG CUGAUGAG X CGAA ACGCCCUC	17	GAGGGCGT T CGTCCTGG	1262
149	CCCAGGAC CUGAUGAG X CGAA AACGCCCU	18	AGGGCGTT C GTCCTGGG	1263
152	GCUCCCAG CUGAUGAG X CGAA ACGAACGC	19	GCGTTCGT C CTGGGAGC	1264
167	GACGGAGC CUGAUGAG X CGAA AGUGCAGC	20	GCTGCACT T GCTCCGTC	1265
171	ACCCGACG CUGAUGAG X CGAA AGCAAGUG	21	CACTTGCT C CGTCGGGT	1266
175	GGCGACCC CUGAUGAG X CGAA ACGGAGCA	22	TGCTCCGT C GGGTCGCC	1267
180	AAGCCGGC CUGAUGAG X CGAA ACCCGACG	23	CGTCGGGT C GCCGGCTT	1268
188	GUCCGGUG CUGAUGAG X CGAA AGCCGGCG	24	CGCCGGCT T CACCGGAC	1269
189	GGUCCGGU CUGAUGAG X CGAA AAGCCGGC	25	GCCGGCTT C ACCGGACC	1270
205	UGCCCCGG CUGAUGAG X CGAA AGCCUGCG	26	CGCAGGCT C CCGGGGCA	1271
231	CGACACGC CUGAUGAG X CGAA AGCUCUGG	27	CCAGAGCT C GCGTGTCG	1272

238	GUCCCGCC CUGAUGAG X CGAA ACACGCGA	28	TCGCGTGT C GGCGGGAC	1273
258	UUAGAGGC CUGAUGAG X CGAA ACGCAGCG	29	CGCTGCGT C GCCTCTAA	1274
263	CGAGGUUA CUGAUGAG X CGAA AGGCGACG	30	CGTCGCCT C TAACCTCG	1275
265	CCCGAGGU CUGAUGAG X CGAA AGAGGCGA	31	TCGCCTCT A ACCTCGGG	1276
270	CACAGCCC CUGAUGAG X CGAA AGGUUAGA	32	TCTAACCT C GGGCTGTG	1277
281	UGGAAAAA CUGAUGAG X CGAA AGCACAGC	33	GCTGTGCT C TTTTTCCA	1278
283	CCUGGAAA CUGAUGAG X CGAA AGAGCACA	34	TGTGCTCT T TTTCCAGG	1279
284	ACCUGGAA CUGAUGAG X CGAA AAGAGCAC	35	GTGCTCTT T TTCCAGGT	1280
285	CACCUGGA CUGAUGAG X CGAA AAAGAGCA	36	TGCTCTTT T TCCAGGTG	1281
286	CCACCUGG CUGAUGAG X CGAA AAAAGAGC	37	GCTCTTTT T CCAGGTGG	1282
287	GCCACCUG CUGAUGAG X CGAA AAAAAGAG	38	CTCTTTTT C CAGGTGGC	1283
304	GGCUCAGA CUGAUGAG X CGAA ACCGGCGG	39	CCGCCGGT T TCTGAGCC	1284
305	AGGCUCAG CUGAUGAG X CGAA AACCGGCG	40	CGCCGGTT T CTGAGCCT	1285
306	AAGGCUCA CUGAUGAG X CGAA AAACCGGC	41	GCCGGTTT C TGAGCCTT	1286
314	CAGGGCAG CUGAUGAG X CGAA AGGCUCAG	42	CTGAGCCT T CTGCCCTG	1287
315	GCAGGGCA CUGAUGAG X CGAA AAGGCUCA	43	TGAGCCTT C TGCCCTGC	1288
335	AGGGUGCA CUGAUGAG X CGAA ACCGUGUC	44	GACACGGT C TGCACCCT	1289
375	UUGGUGUG CUGAUGAG X CGAA AGGGUCAU	45	ATGACCCT C CACACCAA	1290
389	CCAUCCCA CUGAUGAG X CGAA AUGCUUUG	46	CAAAGCAT C TGGGATGG	1291
402	UGAUGCAG CUGAUGAG X CGAA AGGGCCAU	47	ATGGCCCT A CTGCATCA	1292
409	UUGGAUCU CUGAUGAG X CGAA AUGCAGUA	48	TACTGCAT C AGATCCAA	1293
414	UUCCCUUG CUGAUGAG X CGAA AUCUGAUG	49	CATCAGAT C CAAGGGAA	1294
445	GAGCUGCG CUGAUGAG X CGAA ACGGUUCA	50	TGAACCGT C CGCAGCTC	1295
453	GGGAUCUU CUGAUGAG X CGAA AGCUGCGG	51	CCGCAGCT C AAGATCCC	1296
459	UCCAGGGG CUGAUGAG X CGAA AUCUUGAG	52	CTCAAGAT C CCCCTGGA	1297
488	UGUCCAGG CUGAUGAG X CGAA ACACCUCG	53	CGAGGTGT A CCTGGACA	1298
515	GGUAGUUG CUGAUGAG X CGAA ACACGGCG	54	CGCCGTGT A CAACTACC	1299
521	CCUCGGGG CUGAUGAG X CGAA AGUUGUAC	55	GTACAACT A CCCCGAGG	1300
539	UGAACUCG CUGAUGAG X CGAA AGGCGGCG	56	CGCCGCCT A CGAGTTCA	1301
545	CGGCGUUG CUGAUGAG X CGAA ACUCGUAG	57	CTACGAGT T CAACGCCG	1302
546	GCGGCGUU CUGAUGAG X CGAA AACUCGUA	58	TACGAGTT C AACGCCGC	1303

576	UGACCGUA CUGAUGAG X CGAA ACCUGCGC	59	GCGCAGGT C TACGGTCA	1304
578	UCUGACCG CUGAUGAG X CGAA AGACCUGC	60	GCAGGTCT A CGGTCAGA	1305
583	GCCGGUCU CUGAUGAG X CGAA ACCGUAGA	61	TCTACGGT C AGACCGGC	1306
594	CCGUAGGG CUGAUGAG X CGAA AGGCCGGU	62	ACCGGCCT C CCCTACGG	1307
599	CGGGGCCG CUGAUGAG X CGAA AGGGGAGG	63	CCTCCCCT A CGGCCCCG	1308
611	CAGCCUCA CUGAUGAG X CGAA ACCCGGGG	64	CCCCGGGT C TGAGGCTG	1309
626	UGGAGCCG CUGAUGAG X CGAA ACGCCGCA	65	TGCGGCGT T CGGCTCCA	1310
627	UUGGAGCC CUGAUGAG X CGAA AACGCCGC	66	GCGGCGTT C GGCTCCAA	1311
632	GGCCGUUG CUGAUGAG X CGAA AGCCGAAC	67	GTTCGGCT C CAACGGCC	1312
649	UGGGGGGA CUGAUGAG X CGAA ACCCCCCA	68	TGGGGGGT T TCCCCCCA	1313
650	GUGGGGGG CUGAUGAG X CGAA AACCCCCC	69	GGGGGGTT T CCCCCCAC	1314
651	AGUGGGGG CUGAUGAG X CGAA AAACCCCC	70	GGGGGTTT C CCCCCACT	1315
660	ACGCUGUU CUGAUGAG X CGAA AGUGGGGG	71	CCCCCACT C AACAGCGT	1316
671	GGCUCGGA CUGAUGAG X CGAA ACACGCUG	72	CAGCGTGT C TCCGAGCC	1317
673	CGGGCUCG CUGAUGAG X CGAA AGACACGC	73	GCGTGTCT C CGAGCCCG	1318
690	GGGUGCAG CUGAUGAG X CGAA AGCAUCAG	74	CTGATGCT A CTGCACCC	1319
713	GGAAAGGC CUGAUGAG X CGAA ACAGCUGC	75	GCAGCTGT C GCCTTTCC	1320
718	CUGCAGGA CUGAUGAG X CGAA AGGCGACA	76	TGTCGCCT T TCCTGCAG	1321
719	GCUGCAGG CUGAUGAG X CGAA AAGGCGAC	77	GTCGCCTT T CCTGCAGC	1322
720	GGCUGCAG CUGAUGAG X CGAA AAAGGCGA	78	TCGCCTTT C CTGCAGCC	1323
749	CCAGGUAG CUGAUGAG X CGAA AGGGCACC	79	GGTGCCCT A CTACCTGG	1324
752	UCUCCAGG CUGAUGAG X CGAA AGUAGGGC	80	GCCCTACT A CCTGGAGA	1325
776	GCACCGUG CUGAUGAG X CGAA AGCCGCUG	81	CAGCGGCT A CACGGTGC	1326
806	GCCUGUAG CUGAUGAG X CGAA AUGCCGGC	82	GCCGGCAT T CTACAGGC	1327
807	GGCCUGUA CUGAUGAG X CGAA AAUGCCGG	83	CCGGCATT C TACAGGCC	1328
809	UUGGCCUG CUGAUGAG X CGAA AGAAUGCC	84	GGCATTCT A CAGGCCAA	1329
820	AUUAUCUG CUGAUGAG X CGAA AUUUGGCC	85	GGCCAAAT T CAGATAAT	1330
821	GAUUAUCU CUGAUGAG X CGAA AAUUUGGC	86	GCCAAATT C AGATAATC	1331
826	GCGUCGAU CUGAUGAG X CGAA AUCUGAAU	87	ATTCAGAT A ATCGACGC	1332
829	CUGGCGUC CUGAUGAG X CGAA AUUAUCUG	88	CAGATAAT C GACGCCAG	1333
854	UACUGGCC CUGAUGAG X CGAA AUCUUUCU	89	AGAAAGAT T GGCCAGTA	1334

862	GUCAUUGG CUGAUGAG X CGAA ACUGGCCA	90	TGGCCAGT A CCAATGAC	1335
880	CAUAGCCA CUGAUGAG X CGAA ACUUCCCU	91	AGGGAAGT A TGGCTATG	1336
886	AGAUUCCA CUGAUGAG X CGAA AGCCAUAC	92	GTATGGCT A TGGAATCT	1337
893	CCUUGGCA CUGAUGAG X CGAA AUUCCAUA	93	TATGGAAT C TGCCAAGG	1338
907	ACAGUAGC CUGAUGAG X CGAA AGUCUCCU	94	AGGAGACT C GCTACTGT	1339
911	CUGCACAG CUGAUGAG X CGAA AGCGAGUC	95	GACTCGCT A CTGTGCAG	1340
932	CUGAAGCA CUGAUGAG X CGAA AGUCAUUG	96	CAATGACT A TGCTTCAG	1341
937	GUAGCCUG CUGAUGAG X CGAA AGCAUAGU	97	ACTATGCT T CAGGCTAC	1342
938	GGUAGCCU CUGAUGAG X CGAA AAGCAUAG	98	CTATGCTT C AGGCTACC	1343
944	CAUAAUGG CUGAUGAG X CGAA AGCCUGAA	99	TTCAGGCT A CCATTATG	1344
949	GACUCCAU CUGAUGAG X CGAA AUGGUAGC	100	GCTACCAT T ATGGAGTC	1345
950	AGACUCCA CUGAUGAG X CGAA AAUGGUAG	101	CTACCATT A TGGAGTCT	1346
957	CAGGACCA CUGAUGAG X CGAA ACUCCAUA	102	TATGGAGT C TGGTCCTG	1347
962	CCUCACAG CUGAUGAG X CGAA ACCAGACU	103	AGTCTGGT C CTGTGAGG	1348
983	UCUUGAAG CUGAUGAG X CGAA AGGCCUUG	104	CAAGGCCT T CTTCAAGA	1349
984	CUCUUGAA CUGAUGAG X CGAA AAGGCCUU	105	AAGGCCTT C TTCAAGAG	1350
986	UUCUCUUG CUGAUGAG X CGAA AGAAGGCC	106	GGCCTTCT T CAAGAGAA	1351
987	CUUCUCUU CUGAUGAG X CGAA AAGAAGGC	107	GCCTTCTT C AAGAGAAG	1352
997	UCCUUGAA CUGAUGAG X CGAA ACUUCUCU	108	AGAGAAGT A TTCAAGGA	1353
999	UGUCCUUG CUGAUGAG X CGAA AUACUUCU	109	AGAAGTAT T CAAGGACA	1354
1000	AUGUCCUU CUGAUGAG X CGAA AAUACUUC	110	GAAGTATT C AAGGACAT	1355
1009	AUAGUCGU CUGAUGAG X CGAA AUGUCCUU	111	AAGGACAT A ACGACTAT	1356
1016	GACACAUA CUGAUGAG X CGAA AGUCGUUA	112	TAACGACT A TATGTGTC	1357
1018	UGGACACA CUGAUGAG X CGAA AUAGUCGU	113	ACGACTAT A TGTGTCCA	1358
1024	GGUGGCUG CUGAUGAG X CGAA ACACAUAU	114	ATATGTGT C CAGCCACC	1359
1047	UUUUUAUC CUGAUGAG X CGAA AUGGUGCA	115	TGCACCAT T GATAAAAA	1360
1051	CCUGUUUU CUGAUGAG X CGAA AUCAAUGG	116	CCATTGAT A AAAACAGG	1361
1086	CAUUUGCG CUGAUGAG X CGAA AGCCGGCA	117	TGCCGGCT C CGCAAATG	1362
1097	CCACUUCG CUGAUGAG X CGAA AGCAUUUG	118	CAAATGCT A CGAAGTGG	1363
1125	UCUUUUCG CUGAUGAG X CGAA AUCCCACC	119	GGTGGGAT A CGAAAAGA	1364
1154	UGUGUUUC CUGAUGAG X CGAA ACAUUCUC	120	GAGAATGT T GAAACACA	1365

1205	CUCCAGCA CUGAUGAG X CGAA ACCCCACU	121	AGTGGGGT C TGCTGGAG	1366
1233	CUUGGCCA CUGAUGAG X CGAA AGGUUGGC	122	GCCAACCT T TGGCCAAG	1367
1234	GCUUGGCC CUGAUGAG X CGAA AAGGUUGG	123	CCAACCTT T GGCCAAGC	1368
1248	UUGAUCAU CUGAUGAG X CGAA AGCGGGCU	124	AGCCCGCT C ATGATCAA	1369
1254	GAGCGUUU CUGAUGAG X CGAA AUCAUGAG	125	CTCATGAT C AAACGCTC	1370
1262	UCUUCUUA CUGAUGAG X CGAA AGCGUUUG	126	CAAACGCT C TAAGAAGA	1371
1264	GUUCUUCU CUGAUGAG X CGAA AGAGCGUU	127	AACGCTCT A AGAAGAAC	1372
1283	UCAGGGAC CUGAUGAG X CGAA AGGCCAGG	128	CCTGGCCT T GTCCCTGA	1373
1286	CCGUCAGG CUGAUGAG X CGAA ACAAGGCC	129	GGCCTTGT C CCTGACGG	1374
1308	AAGGCACU CUGAUGAG X CGAA ACCAUCUG	130	CAGATGGT C AGTGCCTT	1375
1316	CAUCCAAC CUGAUGAG X CGAA AGGCACUG	131	CAGTGCCT T GTTGGATG	1376
1319	CAGCAUCC CUGAUGAG X CGAA ACAAGGCA	132	TGCCTTGT T GGATGCTG	1377
1338	GAAUAGAG CUGAUGAG X CGAA AUGGGGGG	133	CCCCCCAT A CTCTATTC	1378
1341	UCGGAAUA CUGAUGAG X CGAA AGUAUGGG	134	CCCATACT C TATTCCGA	1379
1343	ACUCGGAA CUGAUGAG X CGAA AGAGUAUG	135	CATACTCT A TTCCGAGT	1380
1345	AUACUCGG CUGAUGAG X CGAA AUAGAGUA	136	TACTCTAT T CCGAGTAT	1381
1346	CAUACUCG CUGAUGAG X CGAA AAUAGAGU	137	ACTCTATT C CGAGTATG	1382
1352	UAGGAUCA CUGAUGAG X CGAA ACUCGGAA	138	TTCCGAGT A TGATCCTA	1383
1357	UCUGGUAG CUGAUGAG X CGAA AUCAUACU	139	AGTATGAT C CTACCAGA	1384
1360	GGGUCUGG CUGAUGAG X CGAA AGGAUCAU	140	ATGATCCT A CCAGACCC	1385
1370	CUUCACUG CUGAUGAG X CGAA AGGGUCUG	141	CAGACCCT T CAGTGAAG	1386
1371	GCUUCACU CUGAUGAG X CGAA AAGGGUCU	142	AGACCCTT C AGTGAAGC	1387
1381	CAUCAUCG CUGAUGAG X CGAA AGCUUCAC	143	GTGAAGCT T CGATGATG	1388
1382	CCAUCAUC CUGAUGAG X CGAA AAGCUUCA	144	TGAAGCTT C GATGATGG	1389
1394	UGGUCAGU CUGAUGAG X CGAA AGCCCAUC	145	GATGGGCT T ACTGACCA	1390
1395	UUGGUCAG CUGAUGAG X CGAA AAGCCCAU	146	ATGGGCTT A CTGACCAA	1391
1425	AUCAUGUG CUGAUGAG X CGAA ACCAGCUC	147	GAGCTGGT T CACATGAT	1392
1426	GAUCAUGU CUGAUGAG X CGAA AACCAGCU	148	AGCTGGTT C ACATGATC	1393
1434	GCCCAGUU CUGAUGAG X CGAA AUCAUGUG	149	CACATGAT C AACTGGGC	1394
1460	AAUCCACA CUGAUGAG X CGAA AGCCUGGC	150	GCCAGGCT T TGTGGATT	1395
1461	AAAUCCAC CUGAUGAG X CGAA AAGCCUGG	151	CCAGGCTT T GTGGATTT	1396

1468	GAGGGUCA CUGAUGAG X CGAA AUCCACAA	152	TTGTGGAT T TGACCCTC	1397
1469	GGAGGGUC CUGAUGAG X CGAA AAUCCACA	153	TGTGGATT T GACCCTCC	1398
1476	UGAUCAUG CUGAUGAG X CGAA AGGGUCAA	154	TTGACCCT C CATGATCA	1399
1483	GUGGACCU CUGAUGAG X CGAA AUCAUGGA	155	TCCATGAT C AGGTCCAC	1400
1488	AGAAGGUG CUGAUGAG X CGAA ACCUGAUC	156	GATCAGGT C CACCTTCT	1401
1494	CAUUCUAG CUGAUGAG X CGAA AGGUGGAC	157	GTCCACCT T CTAGAATG	1402
1495	ACAUUCUA CUGAUGAG X CGAA AAGGUGGA	158	TCCACCTT C TAGAATGT	1403
1497	GCACAUUC CUGAUGAG X CGAA AGAAGGUG	159	CACCTTCT A GAATGTGC	1404
1512	AGGAUCUC CUGAUGAG X CGAA AGCCAGGC	160	GCCTGGCT A GAGATCCT	1405
1518	AUCAUCAG CUGAUGAG X CGAA AUCUCUAG	161	CTAGAGAT C CTGATGAT	1406
1527	ACGAGACC CUGAUGAG X CGAA AUCAUCAG	162	CTGATGAT T GGTCTCGT	1407
1531	CCAGACGA CUGAUGAG X CGAA ACCAAUCA	163	TGATTGGT C TCGTCTGG	1408
1533	CGCCAGAC CUGAUGAG X CGAA AGACCAAU	164	ATTGGTCT C GTCTGGCG	1409
1536	GAGCGCCA CUGAUGAG X CGAA ACGAGACC	165	GGTCTCGT C TGGCGCTC	1410
1544	GCUCCAUG CUGAUGAG X CGAA AGCGCCAG	166	CTGGCGCT C CATGGAGC	1411
1566	GCAAACAG CUGAUGAG X CGAA AGCUUCAC	167	GTGAAGCT A CTGTTTGC	1412
1571	UAGGAGCA CUGAUGAG X CGAA ACAGUAGC	168	GCTACTGT T TGCTCCTA	1413
1572	UUAGGAGC CUGAUGAG X CGAA AACAGUAG	169	CTACTGTT T GCTCCTAA	1414
1576	CAAGUUAG CUGAUGAG X CGAA AGCAAACA	170	TGTTTGCT C CTAACTTG	1415
1579	GAGCAAGU CUGAUGAG X CGAA AGGAGCAA	171	TTGCTCCT A ACTTGCTC	1416
1583	CCAAGAGC CUGAUGAG X CGAA AGUUAGGA	172	TCCTAACT T GCTCTTGG	1417
1587	CUGUCCAA CUGAUGAG X CGAA AGCAAGUU	173	AACTTGCT C TTGGACAG	1418
1589	UCCUGUCC CUGAUGAG X CGAA AGAGCAAG	174	CTTGCTCT T GGACAGGA	1419
1614	AUGCCCUC CUGAUGAG X CGAA ACACAUUU	175	AAATGTGT A GAGGGCAT	1420
1632	AUGUCGAA CUGAUGAG X CGAA AUCUCCAC	176	GTGGAGAT C TTCGACAT	1421
1634	GCAUGUCG CUGAUGAG X CGAA AGAUCUCC	177	GGAGATCT T CGACATGC	1422
1635	AGCAUGUC CUGAUGAG X CGAA AAGAUCUC	178	GAGATCTT C GACATGCT	1423
1651	AGAUGAUG CUGAUGAG X CGAA AGCCAGCA	179	TGCTGGCT A CATCATCT	1424
1655	ACCGAGAU CUGAUGAG X CGAA AUGUAGCC	180	GGCTACAT C ATCTCGGT	1425
1658	GGAACCGA CUGAUGAG X CGAA AUGAUGUA	181	TACATCAT C TCGGTTCC	1426
1660	GCGGAACC CUGAUGAG X CGAA AGAUGAUG	182	CATCATCT C GGTTCCGC	1427

1664	UCAUGCGG CUGAUGAG X CGAA ACCGAGAU	183	ATCTCGGT T CCGCATGA	1428
1665	AUCAUGCG CUGAUGAG X CGAA AACCGAGA	184	TCTCGGTT C CGCATGAT	1429
1678	UCCCUGCA CUGAUGAG X CGAA AUUCAUCA	185	TGATGAAT C TGCAGGGA	1430
1694	GGCACACA CUGAUGAG X CGAA ACUCCUCU	186	AGAGGAGT T TGTGTGCC	1431
1695	AGGCACAC CUGAUGAG X CGAA AACUCCUC	187	GAGGAGTT T GTGTGCCT	1432
1704	AUAGAUUU CUGAUGAG X CGAA AGGCACAC	188	GTGTGCCT C AAATCTAT	1433
1709	AAAUAAUA CUGAUGAG X CGAA AUUUGAGG	189	CCTCAAAT C TATTATTT	1434
1711	CAAAAUAA CUGAUGAG X CGAA AGAUUUGA	190	TCAAATCT A TTATTTTG	1435
1713	AGCAAAAU CUGAUGAG X CGAA AUAGAUUU	191	AAATCTAT T ATTTTGCT	1436
1714	AAGCAAAA CUGAUGAG X CGAA AAUAGAUU	192	AATCTATT A TTTTGCTT	1437
1716	UUAAGCAA CUGAUGAG X CGAA AUAAUAGA	193	TCTATTAT T TTGCTTAA	1438
1717	AUUAAGCA CUGAUGAG X CGAA AAUAAUAG	194	CTATTATT T TGCTTAAT	1439
1718	AAUUAAGC CUGAUGAG X CGAA AAAUAAUA	195	TATTATTT T GCTTAATT	1440
1722	CCAGAAUU CUGAUGAG X CGAA AGCAAAAU	196	ATTTTGCT T AATTCTGG	1441
1723	UCCAGAAU CUGAUGAG X CGAA AAGCAAAA	197	TTTTGCTT A ATTCTGGA	1442
1726	CACUCCAG CUGAUGAG X CGAA AUUAAGCA	198	TGCTTAAT T CTGGAGTG	1443
1727	ACACUCCA CUGAUGAG X CGAA AAUUAAGC	199	GCTTAATT C TGGAGTGT	1444
1736	GAAAUGUG CUGAUGAG X CGAA ACACUCCA	200	TGGAGTGT A CACATTTC	1445
1742	UGGACAGA CUGAUGAG X CGAA AUGUGUAC	201	GTACACAT T TCTGTCCA	1446
1743	CUGGACAG CUGAUGAG X CGAA AAUGUGUA	202	TACACATT T CTGTCCAG	1447
1744	GCUGGACA CUGAUGAG X CGAA AAAUGUGU	203	ACACATTT C TGTCCAGC	1448
1748	GGGUGCUG CUGAUGAG X CGAA ACAGAAAU	204	ATTTCTGT C CAGCACCC	1449
1763	CUUCCAGA CUGAUGAG X CGAA ACUUCAGG	205	CCTGAAGT C TCTGGAAG	1450
1765	CUCUUCCA CUGAUGAG X CGAA AGACUUCA	206	TGAAGTCT C TGGAAGAG	1451
1783	UCGGUGGA CUGAUGAG X CGAA AUGGUCCU	207	AGGACCAT A TCCACCGA	1452
1785	ACUCGGUG CUGAUGAG X CGAA AUAUGGUC	208	GACCATAT C CACCGAGT	1453
1794	UUGUCCAG CUGAUGAG X CGAA ACUCGGUG	209	CACCGAGT C CTGGACAA	1454
1806	GUGUCUGU CUGAUGAG X CGAA AUCUUGUC	210	GACAAGAT C ACAGACAC	1455
1816	GUGGAUCA CUGAUGAG X CGAA AGUGUCUG	211	CAGACACT T TGATCCAC	1456
1817	GGUGGAUC CUGAUGAG X CGAA AAGUGUCU	212	AGACACTT T GATCCACC	1457
1821	AUCAGGUG CUGAUGAG X CGAA AUCAAAGU	213	ACTTTGAT C CACCTGAT	1458

1881	AUGAGGAG CUGAUGAG X CGAA AGCUGGGC	214	GCCCAGCT C CTCCTCAT	1459
1884	AGGAUGAG CUGAUGAG X CGAA AGGAGCUG	215	CAGCTCCT C CTCATCCT	1460
1887	GAGAGGAU CUGAUGAG X CGAA AGGAGGAG	216	CTCCTCCT C ATCCTCTC	1461
1890	UGGGAGAG CUGAUGAG X CGAA AUGAGGAG	217	CTCCTCAT C CTCTCCCA	1462
1893	AUGUGGGA CUGAUGAG X CGAA AGGAUGAG	218	CTCATCCT C TCCCACAT	1463
1895	UGAUGUGG CUGAUGAG X CGAA AGAGGAUG	219	CATCCTCT C CCACATCA	1464
1902	AUGUGCCU CUGAUGAG X CGAA AUGUGGGA	220	TCCCACAT C AGGCACAT	1465
1915	GCCUUUGU CUGAUGAG X CGAA ACUCAUGU	221	ACATGAGT A ACAAAGGC	1466
1933	GCUGUACA CUGAUGAG X CGAA AUGCUCCA	222	TGGAGCAT C TGTACAGC	1467
1937	UCAUGCUG CUGAUGAG X CGAA ACAGAUGC	223	GCATCTGT A CAGCATGA	1468
1968	AGGUCAUA CUGAUGAG X CGAA AGGGGCAC	224	GTGCCCCT C TATGACCT	1469
1970	GCAGGUCA CUGAUGAG X CGAA AGAGGGGC	225	GCCCCTCT A TGACCTGC	1470
2007	GGCGCAUG CUGAUGAG X CGAA AGGCGGUG	226	CACCGCCT A CATGCGCC	1471
2020	UCCACGGC CUGAUGAG X CGAA AGUGGGCG	227	CGCCCACT A GCCGTGGA	1472
2036	CCUCCACG CUGAUGAG X CGAA AUGCCCCU	228	AGGGGCAT C CGTGGAGG	1473
2063	CAGUGGCC CUGAUGAG X CGAA AGUGGCUU	229	AAGCCACT T GGCCACTG	1474
2078	AUGAAGUA CUGAUGAG X CGAA AGCCCGCA	230	TGCGGGCT C TACTTCAT	1475
2080	CGAUGAAG CUGAUGAG X CGAA AGAGCCCG	231	CGGGCTCT A CTTCATCG	1476
2083	AUGCGAUG CUGAUGAG X CGAA AGUAGAGC	232	GCTCTACT T CATCGCAT	1477
2084	AAUGCGAU CUGAUGAG X CGAA AAGUAGAG	233	CTCTACTT C ATCGCATT	1478
2087	AGGAAUGC CUGAUGAG X CGAA AUGAAGUA	234	TACTTCAT C GCATTCCT	1479
2092	UUGCAAGG CUGAUGAG X CGAA AUGCGAUG	235	CATCGCAT T CCTTGCAA	1480
2093	UUUGCAAG CUGAUGAG X CGAA AAUGCGAU	236	ATCGCATT C CTTGCAAA	1481
2096	ACUUUUGC CUGAUGAG X CGAA AGGAAUGC	237	GCATTCCT T GCAAAAGT	1482
2105	UGAUGUAA CUGAUGAG X CGAA ACUUUUGC	238	GCAAAAGT A TTACATCA	1483
2107	CGUGAUGU CUGAUGAG X CGAA AUACUUUU	239	AAAAGTAT T ACATCACG	1484
2108	CCGUGAUG CUGAUGAG X CGAA AAUACUUU	240	AAAGTATT A CATCACGG	1485
2112	UCCCCCGU CUGAUGAG X CGAA AUGUAAUA	241	TATTACAT C ACGGGGGA	1486
2131	GGCAGGGA CUGAUGAG X CGAA ACCCUCUG	242	CAGAGGGT T TCCCTGCC	1487
2132	UGGCAGGG CUGAUGAG X CGAA AACCCUCU	243	AGAGGGTT T CCCTGCCA	1488
2133	GUGGCAGG CUGAUGAG X CGAA AAACCCUC	244	GAGGGTTT C CCTGCCAC	1489

2145	AGCUCUCA CUGAUGAG X CGAA ACUGUGGC	245	GCCACAGT C TGAGAGCT	1490
2154	GAGCCAGG CUGAUGAG X CGAA AGCUCUCA	246	TGAGAGCT C CCTGGCTC	1491
2162	CCGUGUGG CUGAUGAG X CGAA AGCCAGGG	247	CCCTGGCT C CCACACGG	1492
2172	AUUAUCUG CUGAUGAG X CGAA ACCGUGUG	248	CACACGGT T CAGATAAT	1493
2173	GAUUAUCU CUGAUGAG X CGAA AACCGUGU	249	ACACGGTT C AGATAATC	1494
2178	GCAGGGAU CUGAUGAG X CGAA AUCUGAAC	250	GTTCAGAT A ATCCCTGC	1495
2181	GCAGCAGG CUGAUGAG X CGAA AUUAUCUG	251	CAGATAAT C CCTGCTGC	1496
2192	GAGGGUAA CUGAUGAG X CGAA AUGCAGCA	252	TGCTGCAT T TTACCCTC	1497
2193	UGAGGGUA CUGAUGAG X CGAA AAUGCAGC	253	GCTGCATT T TACCCTCA	1498
2194	AUGAGGGU CUGAUGAG X CGAA AAAUGCAG	254	CTGCATTT T ACCCTCAT	1499
2195	GAUGAGGG CUGAUGAG X CGAA AAAAUGCA	255	TGCATTTT A CCCTCATC	1500
2200	UGCAUGAU CUGAUGAG X CGAA AGGGUAAA	256	TTTACCCT C ATCATGCA	1501
2203	UGGUGCAU CUGAUGAG X CGAA AUGAGGGU	257	ACCCTCAT C ATGCACCA	1502
2214	UUUGGCUA CUGAUGAG X CGAA AGUGGUGC	258	GCACCACT T TAGCCAAA	1503
2215	AUUUGGCU CUGAUGAG X CGAA AAGUGGUG	259	CACCACTT T AGCCAAAT	1504
2216	AAUUUGGC CUGAUGAG X CGAA AAAGUGGU	260	ACCACTTT A GCCAAATT	1505
2224	GGAGACAG CUGAUGAG X CGAA AUUUGGCU	261	AGCCAAAT T CTGTCTCC	1506
2225	AGGAGACA CUGAUGAG X CGAA AAUUUGGC	262	GCCAAATT C TGTCTCCT	1507
2229	AUGCAGGA CUGAUGAG X CGAA ACAGAAUU	263	AATTCTGT C TCCTGCAT	1508
2231	GUAUGCAG CUGAUGAG X CGAA AGACAGAA	264	TTCTGTCT C CTGCATAC	1509
2238	CCGGAGUG CUGAUGAG X CGAA AUGCAGGA	265	TCCTGCAT A CACTCCGG	1510
2243	GCAUGCCG CUGAUGAG X CGAA AGUGUAUG	266	CATACACT C CGGCATGC	1511
2254	UGGUGUUG CUGAUGAG X CGAA AUGCAUGC	267	GCATGCAT C CAACACCA	1512
2269	CAUCUAGA CUGAUGAG X CGAA AGCCAUUG	268	CAATGGCT T TCTAGATG	1513
2270	UCAUCUAG CUGAUGAG X CGAA AAGCCAUU	269	AATGGCTT T CTAGATGA	1514
2271	CUCAUCUA CUGAUGAG X CGAA AAAGCCAU	270	ATGGCTTT C TAGATGAG	1515
2273	CACUCAUC CUGAUGAG X CGAA AGAAAGCC	271	GGCTTTCT A GATGAGTG	1516
2287	AGCAAAUG CUGAUGAG X CGAA AUGGCCAC	272	GTGGCCAT T CATTTGCT	1517
2288	AAGCAAAU CUGAUGAG X CGAA AAUGGCCA	273	TGGCCATT C ATTTGCTT	1518
2291	AGCAAGCA CUGAUGAG X CGAA AUGAAUGG	274	CCATTCAT T TGCTTGCT	1519
2292	GAGCAAGC CUGAUGAG X CGAA AAUGAAUG	275	CATTCATT T GCTTGCTC	1520

2296	AACUGAGC CUGAUGAG X CGAA AGCAAAUG	276	CATTTGCT T GCTCAGTT	1521
2300	UAAGAACU CUGAUGAG X CGAA AGCAAGCA	277	TGCTTGCT C AGTTCTTA	1522
2304	CCACUAAG CUGAUGAG X CGAA ACUGAGCA	278	TGCTCAGT T CTTAGTGG	1523
2305	GCCACUAA CUGAUGAG X CGAA AACUGAGC	279	GCTCAGTT C TTAGTGGC	1524
2307	GUGCCACU CUGAUGAG X CGAA AGAACUGA	280	TCAGTTCT T AGTGGCAC	1525
2308	UGUGCCAC CUGAUGAG X CGAA AAGAACUG	281	CAGTTCTT A GTGGCACA	1526
2318	AGACAGAA CUGAUGAG X CGAA AUGUGCCA	282	TGGCACAT C TTCTGTCT	1527
2320	GAAGACAG CUGAUGAG X CGAA AGAUGUGC	283	GCACATCT T CTGTCTTC	1528
2321	AGAAGACA CUGAUGAG X CGAA AAGAUGUG	284	CACATCTT C TGTCTTCT	1529
2325	CAACAGAA CUGAUGAG X CGAA ACAGAAGA	285	TCTTCTGT C TTCTGTTG	1530
2327	CCCAACAG CUGAUGAG X CGAA AGACAGAA	286	TTCTGTCT T CTGTTGGG	1531
2328	UCCCAACA CUGAUGAG X CGAA AAGACAGA	287	TCTGTCTT C TGTTGGGA	1532
2332	CUGUUCCC CUGAUGAG X CGAA ACAGAAGA	288	TCTTCTGT T GGGAACAG	1533
2351	AGCCUUGG CUGAUGAG X CGAA AUCCCUUU	289	AAAGGGAT T CCAAGGCT	1534
2352	UAGCCUUG CUGAUGAG X CGAA AAUCCCUU	290	AAGGGATT C CAAGGCTA	1535
2360	CAAAGAUU CUGAUGAG X CGAA AGCCUUGG	291	CCAAGGCT A AATCTTTG	1536
2364	GUUACAAA CUGAUGAG X CGAA AUUUAGCC	292	GGCTAAAT C TTTGTAAC	1537
2366	CUGUUACA CUGAUGAG X CGAA AGAUUUAG	293	CTAAATCT T TGTAACAG	1538
2367	GCUGUUAC CUGAUGAG X CGAA AAGAUUUA	294	TAAATCTT T GTAACAGC	1539
2370	AGAGCUGU CUGAUGAG X CGAA ACAAAGAU	295	ATCTTTGT A ACAGCTCT	1540
2377	GGGAAAGA CUGAUGAG X CGAA AGCUGUUA	296	TAACAGCT C TCTTTCCC	1541
2379	GGGGGAAA CUGAUGAG X CGAA AGAGCUGU	297	ACAGCTCT C TTTCCCCC	1542
2381	AAGGGGGA CUGAUGAG X CGAA AGAGAGCU	298	AGCTCTCT T TCCCCCTT	1543
2382	CAAGGGGG CUGAUGAG X CGAA AAGAGAGC	299	GCTCTCTT T CCCCCTTG	1544
2383	GCAAGGGG CUGAUGAG X CGAA AAAGAGAG	300	CTCTCTTT C CCCCTTGC	1545
2389	AACAUAGC CUGAUGAG X CGAA AGGGGGAA	301	TTCCCCCT T GCTATGTT	1546
2393	UAGUAACA CUGAUGAG X CGAA AGCAAGGG	302	CCCTTGCT A TGTTACTA	1547
2397	CGCUUAGU CUGAUGAG X CGAA ACAUAGCA	303	TGCTATGT T ACTAAGCG	1548
2398	ACGCUUAG CUGAUGAG X CGAA AACAUAGC	304	GCTATGTT A CTAAGCGT	1549
2401	CUCACGCU CUGAUGAG X CGAA AGUAACAU	305	ATGTTACT A AGCGTGAG	1550
2413	GCUACGGG CUGAUGAG X CGAA AUCCUCAC	306	GTGAGGAT T CCCGTAGC	1551

2414	AGCUACGG CUGAUGAG X CGAA AAUCCUCA	307	TGAGGATT C CCGTAGCT	1552
2419	UGAAGAGC CUGAUGAG X CGAA ACGGGAAU	308	ATTCCCGT A GCTCTTCA	1553
2423	GCUGUGAA CUGAUGAG X CGAA AGCUACGG	309	CCGTAGCT C TTCACAGC	1554
2425	CAGCUGUG CUGAUGAG X CGAA AGAGCUAC	310	GTAGCTCT T CACAGCTG	1555
2426	UCAGCUGU CUGAUGAG X CGAA AAGAGCUA	311	TAGCTCTT C ACAGCTGA	1556
2438	CAUAGACU CUGAUGAG X CGAA AGUUCAGC	312	GCTGAACT C AGTCTATG	1557
2442	AACCCAUA CUGAUGAG X CGAA ACUGAGUU	313	AACTCAGT C TATGGGTT	1558
2444	CCAACCCA CUGAUGAG X CGAA AGACUGAG	314	CTCAGTCT A TGGGTTGG	1559
2450	UGAGCCCC CUGAUGAG X CGAA ACCCAUAG	315	CTATGGGT T GGGGCTCA	1560
2457	AGUUAUCU CUGAUGAG X CGAA AGCCCCAA	316	TTGGGGCT C AGATAACT	1561
2462	CACAGAGU CUGAUGAG X CGAA AUCUGAGC	317	GCTCAGAT A ACTCTGTG	1562
2466	AAUGCACA CUGAUGAG X CGAA AGUUAUCU	318	AGATAACT C TGTGCATT	1563
2474	GUAGCUUA CUGAUGAG X CGAA AUGCACAG	319	CTGTGCAT T TAAGCTAC	1564
2475	AGUAGCUU CUGAUGAG X CGAA AAUGCACA	320	TGTGCATT T AAGCTACT	1565
2476	AAGUAGCU CUGAUGAG X CGAA AAAUGCAC	321	GTGCATTT A AGCTACTT	1566
2481	UCUACAAG CUGAUGAG X CGAA AGCUUAAA	322	TTTAAGCT A CTTGTAGA	1567
2484	GUCUCUAC CUGAUGAG X CGAA AGUAGCUU	323	AAGCTACT T GTAGAGAC	1568
2487	UGGGUCUC CUGAUGAG X CGAA ACAAGUAG	324	CTACTTGT A GAGACCCA	1569
2508	AAAAUGUC CUGAUGAG X CGAA ACUCUCCA	325	TGGAGAGT A GACATTTT	1570
2514	AGAGGCAA CUGAUGAG X CGAA AUGUCUAC	326	GTAGACAT T TTGCCTCT	1571
2515	CAGAGGCA CUGAUGAG X CGAA AAUGUCUA	327	TAGACATT T TGCCTCTG	1572
2516	UCAGAGGC CUGAUGAG X CGAA AAAUGUCU	328	AGACATTT T GCCTCTGA	1573
2521	GCUUAUCA CUGAUGAG X CGAA AGGCAAAA	329	TTTTGCCT C TGATAAGC	1574
2526	AAAGUGCU CUGAUGAG X CGAA AUCAGAGG	330	CCTCTGAT A AGCACTTT	1575
2533	CAUUUAAA CUGAUGAG X CGAA AGUGCUUA	331	TAAGCACT T TTTAAATG	1576
2534	CCAUUUAA CUGAUGAG X CGAA AAGUGCUU	332	AAGCACTT T TTAAATGG	1577
2535	GCCAUUUA CUGAUGAG X CGAA AAAGUGCU	333	AGCACTTT T TAAATGGC	1578
2536	AGCCAUUU CUGAUGAG X CGAA AAAAGUGC	334	GCACTTTT T AAATGGCT	1579
2537	GAGCCAUU CUGAUGAG X CGAA AAAAAGUG	335	CACTTTTT A AATGGCTC	1580
2545	UAUUCUUA CUGAUGAG X CGAA AGCCAUUU	336	AAATGGCT C TAAGAATA	1581
2547	CUUAUUCU CUGAUGAG X CGAA AGAGCCAU	337	ATGGCTCT A AGAATAAG	1582

2553	CUGUGGCU CUGAUGAG X CGAA AUUCUUAG	338	CTAAGAAT A AGCCACAG	1583
2570	CCACUUUA CUGAUGAG X CGAA AUUCUUUG	339	CAAAGAAT T TAAAGTGG	1584
2571	GCCACUUU CUGAUGAG X CGAA AAUUCUUU	340	AAAGAATT T AAAGTGGC	1585
2572	AGCCACUU CUGAUGAG X CGAA AAAUUCUU	341	AAGAATTT A AAGTGGCT	1586
2581	AAUUAAAG CUGAUGAG X CGAA AGCCACUU	342	AAGTGGCT C CTTTAATT	1587
2584	ACCAAUUA CUGAUGAG X CGAA AGGAGCCA	343	TGGCTCCT T TAATTGGT	1588
2585	CACCAAUU CUGAUGAG X CGAA AAGGAGCC	344	GGCTCCTT T AATTGGTG	1589
2586	UCACCAAU CUGAUGAG X CGAA AAAGGAGC	345	GCTCCTTT A ATTGGTGA	1590
2589	AAGUCACC CUGAUGAG X CGAA AUUAAAGG	346	CCTTTAAT T GGTGACTT	1591
2597	CUUUCUCC CUGAUGAG X CGAA AGUCACCA	347	TGGTGACT T GGAGAAAG	1592
2608	CCUUGACC CUGAUGAG X CGAA AGCUUUCU	348	AGAAAGCT A GGTCAAGG	1593
2612	AAACCCUU CUGAUGAG X CGAA ACCUAGCU	349	AGCTAGGT C AAGGGTTT	1594
2619	CUAUAAUA CUGAUGAG X CGAA ACCCUUGA	350	TCAAGGGT T TATTATAG	1595
2620	GCUAUAAU CUGAUGAG X CGAA AACCCUUG	351	CAAGGGTT T ATTATAGC	1596
2621	UGCUAUAA CUGAUGAG X CGAA AAACCCUU	352	AAGGGTTT A TTATAGCA	1597
2623	GGUGCUAU CUGAUGAG X CGAA AUAAACCC	353	GGGTTTAT T ATAGCACC	1598
2624	GGGUGCUA CUGAUGAG X CGAA AAUAAACC	354	GGTTTATT A TAGCACCC	1599
2626	GAGGGUGC CUGAUGAG X CGAA AUAAUAAA	355	TTTATTAT A GCACCCTC	1600
2634	GAAUACAA CUGAUGAG X CGAA AGGGUGCU	356	AGCACCCT C TTGTATTC	1601
2636	AGGAAUAC CUGAUGAG X CGAA AGAGGGUG	357	CACCCTCT T GTATTCCT	1602
2639	CAUAGGAA CUGAUGAG X CGAA ACAAGAGG	358	CCTCTTGT A TTCCTATG	1603
2641	GCCAUAGG CUGAUGAG X CGAA AUACAAGA	359	TCTTGTAT T CCTATGGC	1604
2642	UGCCAUAG CUGAUGAG X CGAA AAUACAAG	360	CTTGTATT C CTATGGCA	1605
2645	CAUUGCCA CUGAUGAG X CGAA AGGAAUAC	361	GTATTCCT A TGGCAATG	1606
2657	CAUAAAAG CUGAUGAG X CGAA AUGCAUUG	362	CAATGCAT C CTTTTATG	1607
2660	UUUCAUAA CUGAUGAG X CGAA AGGAUGCA	363	TGCATCCT T TTATGAAA	1608
2661	CUUUCAUA CUGAUGAG X CGAA AAGGAUGC	364	GCATCCTT T TATGAAAG	1609
2662	ACUUUCAU CUGAUGAG X CGAA AAAGGAUG	365	CATCCTTT T ATGAAAGT	1610
2663	CACUUUCA CUGAUGAG X CGAA AAAAGGAU	366	ATCCTTTT A TGAAAGTG	1611
2674	UUAAGGUG CUGAUGAG X CGAA ACCACUUU	367	AAAGTGGT A CACCTTAA	1612
2680	AAAGCUUU CUGAUGAG X CGAA AGGUGUAC	368	GTACACCT T AAAGCTTT	1613

2681	AAAAGCUU CUGAUGAG X CGAA AAGGUGUA	369	TACACCTT A AAGCTTTT	1614
2687	UCAUAUAA CUGAUGAG X CGAA AGCUUUAA	370	TTAAAGCT T TTATATGA	1615
2688	GUCAUAUA CUGAUGAG X CGAA AAGCUUUA	371	TAAAGCTT T TATATGAC	1616
2689	AGUCAUAU CUGAUGAG X CGAA AAAGCUUU	372	AAAGCTTT T ATATGACT	1617
2690	CAGUCAUA CUGAUGAG X CGAA AAAAGCUU	373	AAGCTTTT A TATGACTG	1618
2692	UACAGUCA CUGAUGAG X CGAA AUAAAAGC	374	GCTTTTAT A TGACTGTA	1619
2700	UACUCUGC CUGAUGAG X CGAA ACAGUCAU	375	ATGACTGT A GCAGAGTA	1620
2708	UCACCAGA CUGAUGAG X CGAA ACUCUGCU	376	AGCAGAGT A TCTGGTGA	1621
2710	AAUCACCA CUGAUGAG X CGAA AUACUCUG	377	CAGAGTAT C TGGTGATT	1622
2718	GAAUUGAC CUGAUGAG X CGAA AUCACCAG	378	CTGGTGAT T GTCAATTC	1623
2721	AGUGAAUU CUGAUGAG X CGAA ACAAUCAC	379	GTGATTGT C AATTCACT	1624
2725	GGGAAGUG CUGAUGAG X CGAA AUUGACAA	380	TTGTCAAT T CACTTCCC	1625
2726	GGGGAAGU CUGAUGAG X CGAA AAUUGACA	381	TGTCAATT C ACTTCCCC	1626
2730	AUAGGGGG CUGAUGAG X CGAA AGUGAAUU	382	AATTCACT T CCCCCTAT	1627
2731	UAUAGGGG CUGAUGAG X CGAA AAGUGAAU	383	ATTCACTT C CCCCTATA	1628
2737	UAUUCCUA CUGAUGAG X CGAA AGGGGGAA	384	TTCCCCCT A TAGGAATA	1629
2739	UGUAUUCC CUGAUGAG X CGAA AUAGGGGG	385	CCCCCTAT A GGAATACA	1630
2745	GCCCCUUG CUGAUGAG X CGAA AUUCCUAU	386	ATAGGAAT A CAAGGGGC	1631
2772	AACUAGGG CUGAUGAG X CGAA AUCUGCCU	387	AGGCAGAT C CCCTAGTT	1632
2777	UGGCCAAC CUGAUGAG X CGAA AGGGGAUC	388	GATCCCCT A GTTGGCCA	1633
2780	UCUUGGCC CUGAUGAG X CGAA ACUAGGGG	389	CCCCTAGT T GGCCAAGA	1634
2791	GUUAAAAU CUGAUGAG X CGAA AGUCUUGG	390	CCAAGACT T ATTTTAAC	1635
2792	AGUUAAAA CUGAUGAG X CGAA AAGUCUUG	391	CAAGACTT A TTTTAACT	1636
2794	CAAGUUAA CUGAUGAG X CGAA AUAAGUCU	392	AGACTTAT T TTAACTTG	1637
2795	UCAAGUUA CUGAUGAG X CGAA AAUAAGUC	393	GACTTATT T TAACTTGA	1638
2796	AUCAAGUU CUGAUGAG X CGAA AAAUAAGU	394	ACTTATTT T AACTTGAT	1639
2797	UAUCAAGU CUGAUGAG X CGAA AAAAUAAG	395	CTTATTTT A ACTTGATA	1640
2801	AGUGUAUC CUGAUGAG X CGAA AGUUAAAA	396	TTTTAACT T GATACACT	1641
2805	CUGCAGUG CUGAUGAG X CGAA AUCAAGUU	397	AACTTGAT A CACTGCAG	1642
2816	ACACUCUG CUGAUGAG X CGAA AUCUGCAG	398	CTGCAGAT T CAGAGTGT	1643
2817	GACACUCU CUGAUGAG X CGAA AAUCUGCA	399	TGCAGATT C AGAGTGTC	1644

2825	AGCUUCAG CUGAUGAG X CGAA ACACUCUG	400	CAGAGTGT C CTGAAGCT	1645
2834	CAGAGGCA CUGAUGAG X CGAA AGCUUCAG	401	CTGAAGCT C TGCCTCTG	1646
2840	GAAAGCCA CUGAUGAG X CGAA AGGCAGAG	402	CTCTGCCT C TGGCTTTC	1647
2846	UGACCGGA CUGAUGAG X CGAA AGCCAGAG	403	CTCTGGCT T TCCGGTCA	1648
2847	AUGACCGG CUGAUGAG X CGAA AAGCCAGA	404	TCTGGCTT T CCGGTCAT	1649
2848	CAUGACCG CUGAUGAG X CGAA AAAGCCAG	405	CTGGCTTT C CGGTCATG	1650
2853	GAACCCAU CUGAUGAG X CGAA ACCGGAAA	406	TTTCCGGT C ATGGGTTC	1651
2860	UUAACUGG CUGAUGAG X CGAA ACCCAUGA	407	TCATGGGT T CCAGTTAA	1652
2861	AUUAACUG CUGAUGAG X CGAA AACCCAUG	408	CATGGGTT C CAGTTAAT	1653
2866	CAUGAAUU CUGAUGAG X CGAA ACUGGAAC	409	GTTCCAGT T AATTCATG	1654
2867	GCAUGAAU CUGAUGAG X CGAA AACUGGAA	410	TTCCAGTT A ATTCATGC	1655
2870	GAGGCAUG CUGAUGAG X CGAA AUUAACUG	411	CAGTTAAT T CATGCCTC	1656
2871	GGAGGCAU CUGAUGAG X CGAA AAUUAACU	412	AGTTAATT C ATGCCTCC	1657
2878	GUCCAUGG CUGAUGAG X CGAA AGGCAUGA	413	TCATGCCT C CCATGGAC	1658
2889	GCUCUCCA CUGAUGAG X CGAA AGGUCCAU	414	ATGGACCT A TGGAGAGC	1659
2905	CUAAGAUC CUGAUGAG X CGAA ACUUGUUG	415	CAACAAGT T GATCTTAG	1660
2909	UUAACUAA CUGAUGAG X CGAA AUCAACUU	416	AAGTTGAT C TTAGTTAA	1661
2911	ACUUAACU CUGAUGAG X CGAA AGAUCAAC	417	GTTGATCT T AGTTAAGT	1662
2912	GACUUAAC CUGAUGAG X CGAA AAGAUCAA	418	TTGATCTT A GTTAAGTC	1663
2915	GGAGACUU CUGAUGAG X CGAA ACUAAGAU	419	ATCTTAGT T AAGTCTCC	1664
2916	GGGAGACU CUGAUGAG X CGAA AACUAAGA	420	TCTTAGTT A AGTCTCCC	1665
2920	UAUAGGGA CUGAUGAG X CGAA ACUUAACU	421	AGTTAAGT C TCCCTATA	1666
2922	CAUAUAGG CUGAUGAG X CGAA AGACUUAA	422	TTAAGTCT C CCTATATG	1667
2926	CCCUCAUA CUGAUGAG X CGAA AGGGAGAC	423	GTCTCCCT A TATGAGGG	1668
2928	AUCCCUCA CUGAUGAG X CGAA AUAGGGAG	424	CTCCCTAT A TGAGGGAT	1669
2937	CAGGAACU CUGAUGAG X CGAA AUCCCUCA	425	TGAGGGAT A AGTTCCTG	1670
2941	AAAUCAGG CUGAUGAG X CGAA ACUUAUCC	426	GGATAAGT T CCTGATTT	1671
2942	AAAAUCAG CUGAUGAG X CGAA AACUUAUC	427	GATAAGTT C CTGATTTT	1672
2948	AAAACAAA CUGAUGAG X CGAA AUCAGGAA	428	TTCCTGAT T TTTGTTTT	1673
2949	AAAAACAA CUGAUGAG X CGAA AAUCAGGA	429	TCCTGATT T TTGTTTTT	1674
2950	UAAAAACA CUGAUGAG X CGAA AAAUCAGG	430	CCTGATTT T TGTTTTTA	1675

2951	AUAAAAAC CUGAUGAG X CGAA AAAAUCAG	431	CTGATTTT T GTTTTTAT	1676
2954	AAAAUAAA CUGAUGAG X CGAA ACAAAAAU	432	ATTTTTGT T TTTATTTT	1677
2955	AAAAAUAA CUGAUGAG X CGAA AACAAAAA	433	TTTTTGTT T TTATTTTT	1678
2956	CAAAAAUA CUGAUGAG X CGAA AAACAAAA	434	TTTTGTTT T TATTTTTG	1679
2957	ACAAAAAU CUGAUGAG X CGAA AAAACAAA	435	TTTGTTTT T ATTTTTGT	1680
2958	CACAAAAA CUGAUGAG X CGAA AAAAACAA	436	TTGTTTTT A TTTTTGTG	1681
2960	AACACAAA CUGAUGAG X CGAA AUAAAAAC	437	GTTTTTAT T TTTGTGTT	1682
2961	UAACACAA CUGAUGAG X CGAA AAUAAAAA	438	TTTTTATT T TTGTGTTA	1683
2962	GUAACACA CUGAUGAG X CGAA AAAUAAAA	439	TTTTATTT T TGTGTTAC	1684
2963	UGUAACAC CUGAUGAG X CGAA AAAAUAAA	440	TTTATTTT T GTGTTACA	1685
2968	UCUUUUGU CUGAUGAG X CGAA ACACAAAA	441	TTTTGTGT T ACAAAAGA	1686
2969	UUCUUUUG CUGAUGAG X CGAA AACACAAA	442	TTTGTGTT A CAAAAGAA	1687
2984	CAGGGAGG CUGAUGAG X CGAA AGGGCUUU	443	AAAGCCCT C CCTCCCTG	1688
2988	AGUUCAGG CUGAUGAG X CGAA AGGGAGGG	444	CCCTCCCT C CCTGAACT	1689
2997	CUUACUGC CUGAUGAG X CGAA AGUUCAGG	445	CCTGAACT T GCAGTAAG	1690
3003	GCUGACCU CUGAUGAG X CGAA ACUGCAAG	446	CTTGCAGT A AGGTCAGC	1691
3008	CUGAAGCU CUGAUGAG X CGAA ACCUUACU	447	AGTAAGGT C AGCTTCAG	1692
3013	AGGUCCUG CUGAUGAG X CGAA AGCUGACC	448	GGTCAGCT T CAGGACCT	1693
3014	CAGGUCCU CUGAUGAG X CGAA AAGCUGAC	449	GTCAGCTT C AGGACCTG	1694
3024	CCCACUGG CUGAUGAG X CGAA ACAGGUCC	450	GGACCTGT T CCAGTGGG	1695
3025	GCCCACUG CUGAUGAG X CGAA AACAGGUC	451	GACCTGTT C CAGTGGGC	1696
3039	GAUCCAAG CUGAUGAG X CGAA ACAGUGCC	452	GGCACTGT A CTTGGATC	1697
3042	GAAGAUCC CUGAUGAG X CGAA AGUACAGU	453	ACTGTACT T GGATCTTC	1698
3047	GCCGGGAA CUGAUGAG X CGAA AUCCAAGU	454	ACTTGGAT C TTCCCGGC	1699
3049	ACGCCGGG CUGAUGAG X CGAA AGAUCCAA	455	TTGGATCT T CCCGGCGT	1700
3050	CACGCCGG CUGAUGAG X CGAA AAGAUCCA	456	TGGATCTT C CCGGCGTG	1701
3068	CCCUGUGU CUGAUGAG X CGAA AGGCACAC	457	GTGTGCCT T ACACAGGG	1702
3069	CCCCUGUG CUGAUGAG X CGAA AAGGCACA	458	TGTGCCTT A CACAGGGG	1703
3086	CCACAGUG CUGAUGAG X CGAA ACAGUUCA	459	TGAACTGT T CACTGTGG	1704
3087	ACCACAGU CUGAUGAG X CGAA AACAGUUC	460	GAACTGTT C ACTGTGGT	1705
3112	CUACCAUU CUGAUGAG X CGAA ACCCUCAU	461	ATGAGGGT A AATGGTAG	1706

3119	CUUUCAAC CUGAUGAG X CGAA ACCAUUUA	462	TAAATGGT A GTTGAAAG	1707
3122	CUCCUUUC CUGAUGAG X CGAA ACUACCAU	463	ATGGTAGT T GAAAGGAG	1708
3146	CUAAAUGC CUGAUGAG X CGAA ACACCAGG	464	CCTGGTGT T GCATTTAG	1709
3151	CAGGGCUA CUGAUGAG X CGAA AUGCAACA	465	TGTTGCAT T TAGCCCTG	1710
3152	CCAGGGCU CUGAUGAG X CGAA AAUGCAAC	466	GTTGCATT T AGCCCTGG	1711
3153	CCCAGGGC CUGAUGAG X CGAA AAAUGCAA	467	TTGCATTT A GCCCTGGG	1712
3179	UGCACAAG CUGAUGAG X CGAA ACUGUUCA	468	TGAACAGT A CTTGTGCA	1713
3182	UCCUGCAC CUGAUGAG X CGAA AGUACUGU	469	ACAGTACT T GTGCAGGA	1714
3192	GCCACAAC CUGAUGAG X CGAA AUCCUGCA	470	TGCAGGAT T GTTGTGGC	1715
3195	GUAGCCAC CUGAUGAG X CGAA ACAAUCCU	471	AGGATTGT T GTGGCTAC	1716
3202	UUCUCUAG CUGAUGAG X CGAA AGCCACAA	472	TTGTGGCT A CTAGAGAA	1717
3205	UUGUUCUC CUGAUGAG X CGAA AGUAGCCA	473	TGGCTACT A GAGAACAA	1718
3224	UUCUGCCC CUGAUGAG X CGAA ACUUUCCC	474	GGGAAAGT A GGGCAGAA	1719
3240	CAGAACUG CUGAUGAG X CGAA AUCCAGUU	475	AACTGGAT A CAGTTCTG	1720
3245	GUGCUCAG CUGAUGAG X CGAA ACUGUAUC	476	GATACAGT T CTGAGCAC	1721
3246	UGUGCUCA CUGAUGAG X CGAA AACUGUAU	477	ATACAGTT C TGAGCACA	1722
3263	ACCUGAGC CUGAUGAG X CGAA AGUCUGGC	478	GCCAGACT T GCTCAGGT	1723
3267	GGCCACCU CUGAUGAG X CGAA AGCAAGUC	479	GACTTGCT C AGGTGGCC	1724
3293	UUCCUAGG CUGAUGAG X CGAA AGCUGCAG	480	CTGCAGCT A CCTAGGAA	1725
3297	AAUGUUCC CUGAUGAG X CGAA AGGUAGCU	481	AGCTACCT A GGAACATT	1726
3305	CUGCAAGG CUGAUGAG X CGAA AUGUUCCU	482	AGGAACAT T CCTTGCAG	1727
3306	UCUGCAAG CUGAUGAG X CGAA AAUGUUCC	483	GGAACATT C CTTGCAGA	1728
3309	GGGUCUGC CUGAUGAG X CGAA AGGAAUGU	484	ACATTCCT T GCAGACCC	1729
3323	CCAAAGGC CUGAUGAG X CGAA AUGCGGGG	485	CCCCGCAT T GCCTTTGG	1730
3328	CACCCCCA CUGAUGAG X CGAA AGGCAAUG	486	CATTGCCT T TGGGGGTG	1731
3329	GCACCCCC CUGAUGAG X CGAA AAGGCAAU	487	ATTGCCTT T GGGGGTGC	1732
3346	ACCCCAGG CUGAUGAG X CGAA AUCCCAGG	488	CCTGGGAT C CCTGGGGT	1733
3355	AGCUGGAC CUGAUGAG X CGAA ACCCCAGG	489	CCTGGGGT A GTCCAGCT	1734
3358	AAGAGCUG CUGAUGAG X CGAA ACUACCCC	490	GGGGTAGT C CAGCTCTT	1735
3364	AUGAAUAA CUGAUGAG X CGAA AGCUGGAC	491	GTCCAGCT C TTATTCAT	1736
3366	AAAUGAAU CUGAUGAG X CGAA AGAGCUGG	492	CCAGCTCT T ATTCATTT	1737

3367	GAAAUGAA CUGAUGAG X CGAA AAGAGCUG	493	CAGCTCTT A TTCATTTC	1738
3369	GGGAAAUG CUGAUGAG X CGAA AUAAGAGC	494	GCTCTTAT T CATTTCCC	1739
3370	UGGGAAAU CUGAUGAG X CGAA AAUAAGAG	495	CTCTTATT C ATTTCCCA	1740
3373	CGCUGGGA CUGAUGAG X CGAA AUGAAUAA	496	TTATTCAT T TCCCAGCG	1741
3374	ACGCUGGG CUGAUGAG X CGAA AAUGAAUA	497	TATTCATT T CCCAGCGT	1742
3375	CACGCUGG CUGAUGAG X CGAA AAAUGAAU	498	ATTCATTT C CCAGCGTG	1743
3392	CUUCUUCC CUGAUGAG X CGAA ACCAGGGC	499	GCCCTGGT T GGAAGAAG	1744
3408	UACAACUU CUGAUGAG X CGAA ACAGCUGC	500	GCAGCTGT C AAGTTGTA	1745
3413	CUGUCUAC CUGAUGAG X CGAA ACUUGACA	501	TGTCAAGT T GTAGACAG	1746
3416	CAGCUGUC CUGAUGAG X CGAA ACAACUUG	502	CAAGTTGT A GACAGCTG	1747
3428	AUUGUAGG CUGAUGAG X CGAA ACACAGCU	503	AGCTGTGT T CCTACAAT	1748
3429	AAUUGUAG CUGAUGAG X CGAA AACACAGC	504	GCTGTGTT C CTACAATT	1749
3432	GCCAAUUG CUGAUGAG X CGAA AGGAACAC	505	GTGTTCCT A CAATTGGC	1750
3437	GCUGGGCC CUGAUGAG X CGAA AUUGUAGG	506	CCTACAAT T GGCCCAGC	1751
3478	GUGACAGC CUGAUGAG X CGAA ACGGUCCC	507	GGGACCGT T GCTGTCAC	1752
3484	UGAGUAGU CUGAUGAG X CGAA ACAGCAAC	508	GTTGCTGT C ACTACTCA	1753
3488	AGCCUGAG CUGAUGAG X CGAA AGUGACAG	509	CTGTCACT A CTCAGGCT	1754
3491	GUCAGCCU CUGAUGAG X CGAA AGUAGUGA	510	TCACTACT C AGGCTGAC	1755
3511	CGUAAUCU CUGAUGAG X CGAA ACCAGGCC	511	GGCCTGGT C AGATTACG	1756
3516	GCAUACGU CUGAUGAG X CGAA AUCUGACC	512	GGTCAGAT T ACGTATGC	1757
3517	GGCAUACG CUGAUGAG X CGAA AAUCUGAC	513	GTCAGATT A CGTATGCC	1758
3521	CAAGGGCA CUGAUGAG X CGAA ACGUAAUC	514	GATTACGT A TGCCCTTG	1759
3528	AAACCACC CUGAUGAG X CGAA AGGGCAUA	515	TATGCCCT T GGTGGTTT	1760
3535	UAUCUCUA CUGAUGAG X CGAA ACCACCAA	516	TTGGTGGT T TAGAGATA	1761
3536	UUAUCUCU CUGAUGAG X CGAA AACCACCA	517	TGGTGGTT T AGAGATAA	1762
3537	AUUAUCUC CUGAUGAG X CGAA AAACCACC	518	GGTGGTTT A GAGATAAT	1763
3543	UUUUGGAU CUGAUGAG X CGAA AUCUCUAA	519	TTAGAGAT A ATCCAAAA	1764
3546	UGAUUUUG CUGAUGAG X CGAA AUUAUCUC	520	GAGATAAT C CAAAATCA	1765
3553	CAAACCCU CUGAUGAG X CGAA AUUUUGGA	521	TCCAAAAT C AGGGTTTG	1766
3559	CCAAACCA CUGAUGAG X CGAA ACCCUGAU	522	ATCAGGGT T TGGTTTGG	1767
3560	CCCAAACC CUGAUGAG X CGAA AACCCUGA	523	TCAGGGTT T GGTTTGGG	1768

3564	CUUCCCCA CUGAUGAG X CGAA ACCAAACC	524	GGTTTGGT T TGGGGAAG	1769
3565	UCUUCCCC CUGAUGAG X CGAA AACCAAAC	525	GTTTGGTT T GGGGAAGA	1770
3578	AGGGGGAG CUGAUGAG X CGAA AUUUUCUU	526	AAGAAAAT C CTCCCCCT	1771
3581	GGAAGGGG CUGAUGAG X CGAA AGGAUUUU	527	AAAATCCT C CCCCTTCC	1772
3587	GGGGGAGG CUGAUGAG X CGAA AGGGGGAG	528	CTCCCCCT T CCTCCCCC	1773
3588	CGGGGGAG CUGAUGAG X CGAA AAGGGGGA	529	TCCCCCTT C CTCCCCCG	1774
3591	GGGCGGGG CUGAUGAG X CGAA AGGAAGGG	530	CCCTTCCT C CCCCGCCC	1775
3603	CGGUAGGG CUGAUGAG X CGAA ACGGGGCG	531	CGCCCCGT T CCCTACCG	1776
3604	GCGGUAGG CUGAUGAG X CGAA AACGGGGC	532	GCCCCGTT C CCTACCGC	1777
3608	GGAGGCGG CUGAUGAG X CGAA AGGGAACG	533	CGTTCCCT A CCGCCTCC	1778
3615	CAGGAGUG CUGAUGAG X CGAA AGGCGGUA	534	TACCGCCT C CACTCCTG	1779
3620	GCUGGCAG CUGAUGAG X CGAA AGUGGAGG	535	CCTCCACT C CTGCCAGC	1780
3630	AAGGAAAU CUGAUGAG X CGAA AGCUGGCA	536	TGCCAGCT C ATTTCCTT	1781
3633	UUGAAGGA CUGAUGAG X CGAA AUGAGCUG	537	CAGCTCAT T TCCTTCAA	1782
3634	AUUGAAGG CUGAUGAG X CGAA AAUGAGCU	538	AGCTCATT T CCTTCAAT	1783
3635	AAUUGAAG CUGAUGAG X CGAA AAAUGAGC	539	GCTCATTT C CTTCAATT	1784
3638	GGAAAUUG CUGAUGAG X CGAA AGGAAAUG	540	CATTTCCT T CAATTTCC	1785
3639	AGGAAAUU CUGAUGAG X CGAA AAGGAAAU	541	ATTTCCTT C AATTTCCT	1786
3643	UCAAAGGA CUGAUGAG X CGAA AUUGAAGG	542	CCTTCAAT T TCCTTTGA	1787
3644	GUCAAAGG CUGAUGAG X CGAA AAUUGAAG	543	CTTCAATT T CCTTTGAC	1788
3645	GGUCAAAG CUGAUGAG X CGAA AAAUUGAA	544	TTCAATTT C CTTTGACC	1789
3648	AUAGGUCA CUGAUGAG X CGAA AGGAAAUU	545	AATTTCCT T TGACCTAT	1790
3649	UAUAGGUC CUGAUGAG X CGAA AAGGAAAU	546	ATTTCCTT T GACCTATA	1791
3655	UUAGCCUA CUGAUGAG X CGAA AGGUCAAA	547	TTTGACCT A TAGGCTAA	1792
3657	UUUUAGCC CUGAUGAG X CGAA AUAGGUCA	548	TGACCTAT A GGCTAAAA	1793
3662	UUCUUUUU CUGAUGAG X CGAA AGCCUAUA	549	TATAGGCT A AAAAAGAA	1794
3676	GCUGGAAU CUGAUGAG X CGAA AGCCUUUC	550	GAAAGGCT C ATTCCAGC	1795
3679	GUGGCUGG CUGAUGAG X CGAA AUGAGCCU	551	AGGCTCAT T CCAGCCAC	1796
3680	UGUGGCUG CUGAUGAG X CGAA AAUGAGCC	552	GGCTCATT C CAGCCACA	1797
3698	GCCCAGGG CUGAUGAG X CGAA AGGCUGCC	553	GGCAGCCT T CCCTGGGC	1798
3699	GGCCCAGG CUGAUGAG X CGAA AAGGCUGC	554	GCAGCCTT C CCTGGGCC	1799

3709	GAGAAGCA CUGAUGAG X CGAA AGGCCCAG	555	CTGGGCCT T TGCTTCTC	1800
3710	AGAGAAGC CUGAUGAG X CGAA AAGGCCCA	556	TGGGCCTT T GCTTCTCT	1801
3714	UGCUAGAG CUGAUGAG X CGAA AGCAAAGG	557	CCTTTGCT T CTCTAGCA	1802
3715	GUGCUAGA CUGAUGAG X CGAA AAGCAAAG	558	CTTTGCTT C TCTAGCAC	1803
3717	UUGUGCUA CUGAUGAG X CGAA AGAAGCAA	559	TTGCTTCT C TAGCACAA	1804
3719	AAUUGUGC CUGAUGAG X CGAA AGAGAAGC	560	GCTTCTCT A GCACAATT	1805
3727	UAACCCAU CUGAUGAG X CGAA AUUGUGCU	561	AGCACAAT T ATGGGTTA	1806
3728	GUAACCCA CUGAUGAG X CGAA AAUUGUGC	562	GCACAATT A TGGGTTAC	1807
3734	AAGGAAGU CUGAUGAG X CGAA ACCCAUAA	563	TTATGGGT T ACTTCCTT	1808
3735	AAAGGAAG CUGAUGAG X CGAA AACCCAUA	564	TATGGGTT A CTTCCTTT	1809
3738	GAAAAAGG CUGAUGAG X CGAA AGUAACCC	565	GGGTTACT T CCTTTTTC	1810
3739	AGAAAAAG CUGAUGAG X CGAA AAGUAACC	566	GGTTACTT C CTTTTTCT	1811
3742	UUAAGAAA CUGAUGAG X CGAA AGGAAGUA	567	TACTTCCT T TTTCTTAA	1812
3743	GUUAAGAA CUGAUGAG X CGAA AAGGAAGU	568	ACTTCCTT T TTCTTAAC	1813
3744	UGUUAAGA CUGAUGAG X CGAA AAAGGAAG	569	CTTCCTTT T TCTTAACA	1814
3745	UUGUUAAG CUGAUGAG X CGAA AAAAGGAA	570	TTCCTTTT T CTTAACAA	1815
3746	UUUGUUAA CUGAUGAG X CGAA AAAAAGGA	571	TCCTTTTT C TTAACAAA	1816
3748	UUUUUGUU CUGAUGAG X CGAA AGAAAAAG	572	CTTTTTCT T AACAAAAA	1817
3749	UUUUUUGU CUGAUGAG X CGAA AAGAAAAA	573	TTTTTCTT A ACAAAAAA	1818
3764	GGAAAUCA CUGAUGAG X CGAA ACAUUCUU	574	AAGAATGT T TGATTTCC	1819
3765	AGGAAAUC CUGAUGAG X CGAA AACAUUCU	575	AGAATGTT T GATTTCCT	1820
3769	CCAGAGGA CUGAUGAG X CGAA AUCAAACA	576	TGTTTGAT T TCCTCTGG	1821
3770	CCCAGAGG CUGAUGAG X CGAA AAUCAAAC	577	GTTTGATT T CCTCTGGG	1822
3771	ACCCAGAG CUGAUGAG X CGAA AAAUCAAA	578	TTTGATTT C CTCTGGGT	1823
3774	GUCACCCA CUGAUGAG X CGAA AGGAAAUC	579	GATTTCCT C TGGGTGAC	1824
3785	CAGACAAU CUGAUGAG X CGAA AGGUCACC	580	GGTGACCT T ATTGTCTG	1825
3786	ACAGACAA CUGAUGAG X CGAA AAGGUCAC	581	GTGACCTT A TTGTCTGT	1826
3788	UUACAGAC CUGAUGAG X CGAA AUAAGGUC	582	GACCTTAT T GTCTGTAA	1827
3791	CAAUUACA CUGAUGAG X CGAA ACAAUAAG	583	CTTATTGT C TGTAATTG	1828
3795	GUUUCAAU CUGAUGAG X CGAA ACAGACAA	584	TTGTCTGT A ATTGAAAC	1829
3798	AGGGUUUC CUGAUGAG X CGAA AUUACAGA	585	TCTGTAAT T GAAACCCT	1830

3807	CCUCUCAA CUGAUGAG X CGAA AGGGUUUC	586	GAAACCCT A TTGAGAGG	1831
3809	CACCUCUC CUGAUGAG X CGAA AUAGGGUU	587	AACCCTAT T GAGAGGTG	1832
3822	CUAACACA CUGAUGAG X CGAA ACAUCACC	588	GGTGATGT C TGTGTTAG	1833
3828	CAUUGGCU CUGAUGAG X CGAA ACACAGAC	589	GTCTGTGT T AGCCAATG	1834
3829	UCAUUGGC CUGAUGAG X CGAA AACACAGA	590	TCTGTGTT A GCCAATGA	1835
3845	CGAGCAGC CUGAUGAG X CGAA ACCUGGGU	591	ACCCAGGT A GCTGCTCG	1836
3852	AGAAGCCC CUGAUGAG X CGAA AGCAGCUA	592	TAGCTGCT C GGGCTTCT	1837
3858	ACCAAGAG CUGAUGAG X CGAA AGCCCGAG	593	CTCGGGCT T CTCTTGGT	1838
3859	UACCAAGA CUGAUGAG X CGAA AAGCCCGA	594	TCGGGCTT C TCTTGGTA	1839
3861	CAUACCAA CUGAUGAG X CGAA AGAAGCCC	595	GGGCTTCT C TTGGTATG	1840
3863	GACAUACC CUGAUGAG X CGAA AGAGAAGC	596	GCTTCTCT T GGTATGTC	1841
3867	ACAAGACA CUGAUGAG X CGAA ACCAAGAG	597	CTCTTGGT A TGTCTTGT	1842
3871	CCAAACAA CUGAUGAG X CGAA ACAUACCA	598	TGGTATGT C TTGTTTGG	1843
3873	UUCCAAAC CUGAUGAG X CGAA AGACAUAC	599	GTATGTCT T GTTTGGAA	1844
3876	CUUUUCCA CUGAUGAG X CGAA ACAAGACA	600	TGTCTTGT T TGGAAAAG	1845
3877	ACUUUUCC CUGAUGAG X CGAA AACAAGAC	601	GTCTTGTT T GGAAAAGT	1846
3890	AUGAAUGA CUGAUGAG X CGAA AUCCACUU	602	AAGTGGAT T TCATTCAT	1847
3891	AAUGAAUG CUGAUGAG X CGAA AAUCCACU	603	AGTGGATT T CATTCATT	1848
3892	AAAUGAAU CUGAUGAG X CGAA AAAUCCAC	604	GTGGATTT C ATTCATTT	1849
3895	CAGAAAUG CUGAUGAG X CGAA AUGAAAUC	605	GATTTCAT T CATTTCTG	1850
3896	UCAGAAAU CUGAUGAG X CGAA AAUGAAAU	606	ATTTCATT C ATTTCTGA	1851
3899	CAAUCAGA CUGAUGAG X CGAA AUGAAUGA	607	TCATTCAT T TCTGATTG	1852
3900	ACAAUCAG CUGAUGAG X CGAA AAUGAAUG	608	CATTCATT T CTGATTGT	1853
3901	GACAAUCA CUGAUGAG X CGAA AAAUGAAU	609	ATTCATTT C TGATTGTC	1854
3906	AACUGGAC CUGAUGAG X CGAA AUCAGAAA	610	TTTCTGAT T GTCCAGTT	1855
3909	CUUAACUG CUGAUGAG X CGAA ACAAUCAG	611	CTGATTGT C CAGTTAAG	1856
3914	GAUCACUU CUGAUGAG X CGAA ACUGGACA	612	TGTCCAGT T AAGTGATC	1857
3915	UGAUCACU CUGAUGAG X CGAA AACUGGAC	613	GTCCAGTT A AGTGATCA	1858
3922	CCUUUGGU CUGAUGAG X CGAA AUCACUUA	614	TAAGTGAT C ACCAAAGG	1859
3940	CCCUCCCA CUGAUGAG X CGAA AUUCUCAG	615	CTGAGAAT C TGGGAGGG	1860
3968	CACAUAAA CUGAUGAG X CGAA ACUUUUUU	616	AAAAAAGT T TTTATGTG	1861

3969	GCACAUAA CUGAUGAG X CGAA AACUUUUU	617	AAAAAGTT T TTATGTGC	1862
3970	UGCACAUA CUGAUGAG X CGAA AAACUUUU	618	AAAAGTTT T TATGTGCA	1863
3971	GUGCACAU CUGAUGAG X CGAA AAAACUUU	619	AAAGTTTT T ATGTGCAC	1864
3972	AGUGCACA CUGAUGAG X CGAA AAAAACUU	620	AAGTTTTT A TGTGCACT	1865
3981	CCAAAUUU CUGAUGAG X CGAA AGUGCACA	621	TGTGCACT T AAATTTGG	1866
3982	CCCAAAUU CUGAUGAG X CGAA AAGUGCAC	622	GTGCACTT A AATTTGGG	1867
3986	UGUCCCCA CUGAUGAG X CGAA AUUUAAGU	623	ACTTAAAT T TGGGGACA	1868
3987	UUGUCCCC CUGAUGAG X CGAA AAUUUAAG	624	CTTAAATT T GGGGACAA	1869
3997	AUACAUAA CUGAUGAG X CGAA AUUGUCCC	625	GGGACAAT T TTATGTAT	1870
3998	GAUACAUA CUGAUGAG X CGAA AAUUGUCC	626	GGACAATT T TATGTATC	1871
3999	AGAUACAU CUGAUGAG X CGAA AAAUUGUC	627	GACAATTT T ATGTATCT	1872
4000	CAGAUACA CUGAUGAG X CGAA AAAAUUGU	628	ACAATTTT A TGTATCTG	1873
4004	AACACAGA CUGAUGAG X CGAA ACAUAAAA	629	TTTTATGT A TCTGTGTT	1874
4006	UUAACACA CUGAUGAG X CGAA AUACAUAA	630	TTATGTAT C TGTGTTAA	1875
4012	AUAUCCUU CUGAUGAG X CGAA ACACAGAU	631	ATCTGTGT T AAGGATAT	1876
4013	CAUAUCCU CUGAUGAG X CGAA AACACAGA	632	TCTGTGTT A AGGATATG	1877
4019	CUUAAGCA CUGAUGAG X CGAA AUCCUUAA	633	TTAAGGAT A TGCTTAAG	1878
4024	AUGUUCUU CUGAUGAG X CGAA AGCAUAUC	634	GATATGCT T AAGAACAT	1879
4025	UAUGUUCU CUGAUGAG X CGAA AAGCAUAU	635	ATATGCTT A AGAACATA	1880
4033	AAAAGAAU CUGAUGAG X CGAA AUGUUCUU	636	AAGAACAT A ATTCTTTT	1881
4036	AACAAAAG CUGAUGAG X CGAA AUUAUGUU	637	AACATAAT T CTTTTGTT	1882
4037	CAACAAAA CUGAUGAG X CGAA AAUUAUGU	638	ACATAATT C TTTTGTTG	1883
4039	AGCAACAA CUGAUGAG X CGAA AGAAUUAU	639	ATAATTCT T TTGTTGCT	1884
4040	CAGCAACA CUGAUGAG X CGAA AAGAAUUA	640	TAATTCTT T TGTTGCTG	1885
4041	ACAGCAAC CUGAUGAG X CGAA AAAGAAUU	641	AATTCTTT T GTTGCTGT	1886
4044	CAAACAGC CUGAUGAG X CGAA ACAAAAGA	642	TCTTTTGT T GCTGTTTG	1887
4050	CUUAAACA CUGAUGAG X CGAA ACAGCAAC	643	GTTGCTGT T TGTTTAAG	1888
4051	UCUUAAAC CUGAUGAG X CGAA AACAGCAA	644	TTGCTGTT T GTTTAAGA	1889
4054	GCUUCUUA CUGAUGAG X CGAA ACAAACAG	645	CTGTTTGT T TAAGAAGC	1890
4055	UGCUUCUU CUGAUGAG X CGAA AACAAACA	646	TGTTTGTT T AAGAAGCA	1891
4056	GUGCUUCU CUGAUGAG X CGAA AAACAAAC	647	GTTTGTTT A AGAAGCAC	1892

4067	AACAAACU CUGAUGAG X CGAA AGGUGCUU	648	AAGCACCT T AGTTTGTT	1893
4068	AAACAAAC CUGAUGAG X CGAA AAGGUGCU	649	AGCACCTT A GTTTGTTT	1894
4071	CUUAAACA CUGAUGAG X CGAA ACUAAGGU	650	ACCTTAGT T TGTTTAAG	1895
4072	UCUUAAAC CUGAUGAG X CGAA AACUAAGG	651	CCTTAGTT T GTTTAAGA	1896
4075	GCUUCUUA CUGAUGAG X CGAA ACAAACUA	652	TAGTTTGT T TAAGAAGC	1897
4076	UGCUUCUU CUGAUGAG X CGAA AACAAACU	653	AGTTTGTT T AAGAAGCA	1898
4077	GUGCUUCU CUGAUGAG X CGAA AAACAAAC	654	GTTTGTTT A AGAAGCAC	1899
4088	UACUAUAU CUGAUGAG X CGAA AGGUGCUU	655	AAGCACCT T ATATAGTA	1900
4089	AUACUAUA CUGAUGAG X CGAA AAGGUGCU	656	AGCACCTT A TATAGTAT	1901
4091	UUAUACUA CUGAUGAG X CGAA AUAAGGUG	657	CACCTTAT A TAGTATAA	1902
4093	UAUUAUAC CUGAUGAG X CGAA AUAUAAGG	658	CCTTATAT A GTATAATA	1903
4096	AUAUAUUA CUGAUGAG X CGAA ACUAUAUA	659	TATATAGT A TAATATAT	1904
4098	AUAUAUAU CUGAUGAG X CGAA AUACUAUA	660	TATAGTAT A ATATATAT	1905
4101	AAAAUAUA CUGAUGAG X CGAA AUUAUACU	661	AGTATAAT A TATATTTT	1906
4103	AAAAAAUA CUGAUGAG X CGAA AUAUUAUA	662	TATAATAT A TATTTTTT	1907
4105	CAAAAAAA CUGAUGAG X CGAA AUAUAUUA	663	TAATATAT A TTTTTTTG	1908
4107	UUCAAAAA CUGAUGAG X CGAA AUAUAUAU	664	ATATATAT T TTTTTGAA	1909
4108	UUUCAAAA CUGAUGAG X CGAA AAUAUAUA	665	TATATATT T TTTTGAAA	1910
4109	AUUUCAAA CUGAUGAG X CGAA AAAUAUAU	666	ATATATTT T TTTGAAAT	1911
4110	AAUUUCAA CUGAUGAG X CGAA AAAAUAUA	667	TATATTTT T TTGAAATT	1912
4111	UAAUUUCA CUGAUGAG X CGAA AAAAAUAU	668	ATATTTTT T TGAAATTA	1913
4112	GUAAUUUC CUGAUGAG X CGAA AAAAAAUA	669	TATTTTTT T GAAATTAC	1914
4118	AGCAAUGU CUGAUGAG X CGAA AUUUCAAA	670	TTTGAAAT T ACATTGCT	1915
4119	AAGCAAUG CUGAUGAG X CGAA AAUUUCAA	671	TTGAAATT A CATTGCTT	1916
4123	AAACAAGC CUGAUGAG X CGAA AUGUAAUU	672	AATTACAT T GCTTGTTT	1917
4127	UGAUAAAC CUGAUGAG X CGAA AGCAAUGU	673	ACATTGCT T GTTTATCA	1918
4130	GUCUGAUA CUGAUGAG X CGAA ACAAGCAA	674	TTGCTTGT T TATCAGAC	1919
4131	UGUCUGAU CUGAUGAG X CGAA AACAAGCA	675	TGCTTGTT T ATCAGACA	1920
4132	UUGUCUGA CUGAUGAG X CGAA AAACAAGC	676	GCTTGTTT A TCAGACAA	1921
4134	AAUUGUCU CUGAUGAG X CGAA AUAAACAA	677	TTGTTTAT C AGACAATT	1922
4142	CUACAUUC CUGAUGAG X CGAA AUUGUCUG	678	CAGACAAT T GAATGTAG	1923

4149	AGAAUUAC CUGAUGAG X CGAA ACAUUCAA	679	TTGAATGT A GTAATTCT	1924
4152	AACAGAAU CUGAUGAG X CGAA ACUACAUU	680	AATGTAGT A ATTCTGTT	1925
4155	CAGAACAG CUGAUGAG X CGAA AUUACUAC	681	GTAGTAAT T CTGTTCTG	1926
4156	CCAGAACA CUGAUGAG X CGAA AAUUACUA	682	TAGTAATT C TGTTCTGG	1927
4160	AAAUCCAG CUGAUGAG X CGAA ACAGAAUU	683	AATTCTGT T CTGGATTT	1928
4161	UAAAUCCA CUGAUGAG X CGAA AACAGAAU	684	ATTCTGTT C TGGATTTA	1929
4167	UCAAAUUA CUGAUGAG X CGAA AUCCAGAA	685	TTCTGGAT T TAATTTGA	1930
4168	GUCAAAUU CUGAUGAG X CGAA AAUCCAGA	686	TCTGGATT T AATTTGAC	1931
4169	AGUCAAAU CUGAUGAG X CGAA AAAUCCAG	687	CTGGATTT A ATTTGACT	1932
4172	CCCAGUCA CUGAUGAG X CGAA AUUAAAUC	688	GATTTAAT T TGACTGGG	1933
4173	ACCCAGUC CUGAUGAG X CGAA AAUUAAAU	689	ATTTAATT T GACTGGGT	1934
4182	UGCAUGUU CUGAUGAG X CGAA ACCCAGUC	690	GACTGGGT T AACATGCA	1935
4183	UUGCAUGU CUGAUGAG X CGAA AACCCAGU	691	ACTGGGTT A ACATGCAA	1936
4207	AAACUAAA CUGAUGAG X CGAA AUUUUUCC	692	GGAAAAAT A TTTAGTTT	1937
4209	AAAAACUA CUGAUGAG X CGAA AUAUUUUU	693	AAAAATAT T TAGTTTTT	1938
4210	AAAAAACU CUGAUGAG X CGAA AAUAUUUU	694	AAAATATT T AGTTTTTT	1939
4211	AAAAAAAC CUGAUGAG X CGAA AAAUAUUU	695	AAATATTT A GTTTTTTT	1940
4214	AAAAAAAA CUGAUGAG X CGAA ACUAAAUA	696	TATTTAGT T TTTTTTTT	1941
4215	AAAAAAAA CUGAUGAG X CGAA AACUAAAU	697	ATTTAGTT T TTTTTTTT	1942
4216	AAAAAAAA CUGAUGAG X CGAA AAACUAAA	698	TTTAGTTT T TTTTTTTT	1943
4217	AAAAAAAA CUGAUGAG X CGAA AAAACUAA	699	TTAGTTTT T TTTTTTTT	1944
4218	AAAAAAAA CUGAUGAG X CGAA AAAAACUA	700	TAGTTTTT T TTTTTTTT	1945
4219	AAAAAAAA CUGAUGAG X CGAA AAAAAACU	701	AGTTTTTT T TTTTTTTT	1946
4220	AAAAAAAA CUGAUGAG X CGAA AAAAAAAC	702	GTTTTTTT T TTTTTTTT	1947
4221	AAAAAAAA CUGAUGAG X CGAA AAAAAAAA	703	TTTTTTTT T TTTTTTTT	1948
4222	CAAAAAAA CUGAUGAG X CGAA AAAAAAAA	704	TTTTTTTT T TTTTTTTG	1949
4223	ACAAAAAA CUGAUGAG X CGAA AAAAAAAA	705	TTTTTTTT T TTTTTTGT	1950
4224	UACAAAAA CUGAUGAG X CGAA AAAAAAAA	706	TTTTTTTT T TTTTTGTA	1951
4225	AUACAAAA CUGAUGAG X CGAA AAAAAAAA	707	TTTTTTTT T TTTTGTAT	1952
4226	UAUACAAA CUGAUGAG X CGAA AAAAAAAA	708	TTTTTTTT T TTTGTATA	1953
4227	GUAUACAA CUGAUGAG X CGAA AAAAAAAA	709	TTTTTTTT T TTGTATAC	1954

4228	AGUAUACA CUGAUGAG X CGAA AAAAAAAA	710	TTTTTTTT T TGTATACT	1955
4229	AAGUAUAC CUGAUGAG X CGAA AAAAAAAA	711	TTTTTTTT T GTATACTT	1956
4232	GAAAAGUA CUGAUGAG X CGAA ACAAAAAA	712	TTTTTTGT A TACTTTTC	1957
4234	UUGAAAAG CUGAUGAG X CGAA AUACAAAA	713	TTTTGTAT A CTTTTCAA	1958
4237	AGCUUGAA CUGAUGAG X CGAA AGUAUACA	714	TGTATACT T TTCAAGCT	1959
4238	UAGCUUGA CUGAUGAG X CGAA AAGUAUAC	715	GTATACTT T TCAAGCTA	1960
4239	GUAGCUUG CUGAUGAG X CGAA AAAGUAUA	716	TATACTTT T CAAGCTAC	1961
4240	GGUAGCUU CUGAUGAG X CGAA AAAAGUAU	717	ATACTTTT C AAGCTACC	1962
4246	UGACAAGG CUGAUGAG X CGAA AGCUUGAA	718	TTCAAGCT A CCTTGTCA	1963
4250	UACAUGAC CUGAUGAG X CGAA AGGUAGCU	719	AGCTACCT T GTCATGTA	1964
4253	GUAUACAU CUGAUGAG X CGAA ACAAGGUA	720	TACCTTGT C ATGTATAC	1965
4258	UGACUGUA CUGAUGAG X CGAA ACAUGACA	721	TGTCATGT A TACAGTCA	1966
4260	AAUGACUG CUGAUGAG X CGAA AUACAUGA	722	TCATGTAT A CAGTCATT	1967
4265	GCAUAAAU CUGAUGAG X CGAA ACUGUAUA	723	TATACAGT C ATTTATGC	1968
4268	UAGGCAUA CUGAUGAG X CGAA AUGACUGU	724	ACAGTCAT T TATGCCTA	1969
4269	UUAGGCAU CUGAUGAG X CGAA AAUGACUG	725	CAGTCATT T ATGCCTAA	1970
4270	UUUAGGCA CUGAUGAG X CGAA AAAUGACU	726	AGTCATTT A TGCCTAAA	1971
4276	CCAGGCUU CUGAUGAG X CGAA AGGCAUAA	727	TTATGCCT A AAGCCTGG	1972
4289	AAAUGAAU CUGAUGAG X CGAA AUCACCAG	728	CTGGTGAT T ATTCATTT	1973
4290	UAAAUGAA CUGAUGAG X CGAA AAUCACCA	729	TGGTGATT A TTCATTTA	1974
4292	UUUAAAUG CUGAUGAG X CGAA AUAAUCAC	730	GTGATTAT T CATTTAAA	1975
4293	AUUUAAAU CUGAUGAG X CGAA AAUAAUCA	731	TGATTATT C ATTTAAAT	1976
4296	UUCAUUUA CUGAUGAG X CGAA AUGAAUAA	732	TTATTCAT T TAAATGAA	1977
4297	CUUCAUUU CUGAUGAG X CGAA AAUGAAUA	733	TATTCATT T AAATGAAG	1978
4298	UCUUCAUU CUGAUGAG X CGAA AAAUGAAU	734	ATTCATTT A AATGAAGA	1979
4308	UGAAAUGU CUGAUGAG X CGAA AUCUUCAU	735	ATGAAGAT C ACATTTCA	1980
4313	UGAUAUGA CUGAUGAG X CGAA AUGUGAUC	736	GATCACAT T TCATATCA	1981
4314	UUGAUAUG CUGAUGAG X CGAA AAUGUGAU	737	ATCACATT T CATATCAA	1982
4315	GUUGAUAU CUGAUGAG X CGAA AAAUGUGA	738	TCACATTT C ATATCAAC	1983
4318	AAAGUUGA CUGAUGAG X CGAA AUGAAAUG	739	CATTTCAT A TCAACTTT	1984
4320	CAAAAGUU CUGAUGAG X CGAA AUAUGAAA	740	TTTCATAT C AACTTTTG	1985

4325	GGAUACAA CUGAUGAG X CGAA AGUUGAUA	741	TATCAACT T TTGTATCC	1986
4326	UGGAUACA CUGAUGAG X CGAA AAGUUGAU	742	ATCAACTT T TGTATCCA	1987
4327	GUGGAUAC CUGAUGAG X CGAA AAAGUUGA	743	TCAACTTT T GTATCCAC	1988
4330	ACUGUGGA CUGAUGAG X CGAA ACAAAAGU	744	ACTTTTGT A TCCACAGT	1989
4332	CUACUGUG CUGAUGAG X CGAA AUACAAAA	745	TTTTGTAT C CACAGTAG	1990
4339	AUUUUGUC CUGAUGAG X CGAA ACUGUGGA	746	TCCACAGT A GACAAAAT	1991
4348	AUUAGUGC CUGAUGAG X CGAA AUUUUGUC	747	GACAAAAT A GCACTAAT	1992
4354	AUCUGGAU CUGAUGAG X CGAA AGUGCUAU	748	ATAGCACT A ATCCAGAT	1993
4357	GGCAUCUG CUGAUGAG X CGAA AUUAGUGC	749	GCACTAAT C CAGATGCC	1994
4367	UCCAACAA CUGAUGAG X CGAA AGGCAUCU	750	AGATGCCT A TTGTTGGA	1995
4369	UAUCCAAC CUGAUGAG X CGAA AUAGGCAU	751	ATGCCTAT T GTTGGATA	1996
4372	CAAUAUCC CUGAUGAG X CGAA ACAAUAGG	752	CCTATTGT T GGATATTG	1997
4377	UCAUUCAA CUGAUGAG X CGAA AUCCAACA	753	TGTTGGAT A TTGAATGA	1998
4379	UGUCAUUC CUGAUGAG X CGAA AUAUCCAA	754	TTGGATAT T GAATGACA	1999
4394	CUACAUAA CUGAUGAG X CGAA AUUGUCUG	755	CAGACAAT C TTATGTAG	2000
4396	UGCUACAU CUGAUGAG X CGAA AGAUUGUC	756	GACAATCT T ATGTAGCA	2001
4397	UUGCUACA CUGAUGAG X CGAA AAGAUUGU	757	ACAATCTT A TGTAGCAA	2002
4401	AUCUUUGC CUGAUGAG X CGAA ACAUAAGA	758	TCTTATGT A GCAAAGAT	2003
4410	UCAGGCAU CUGAUGAG X CGAA AUCUUUGC	759	GCAAAGAT T ATGCCTGA	2004
4411	UUCAGGCA CUGAUGAG X CGAA AAUCUUUG	760	CAAAGATT A TGCCTGAA	2005
4429	CCCUGAAU CUGAUGAG X CGAA AUUUUCCU	761	AGGAAAAT T ATTCAGGG	2006
4430	GCCCUGAA CUGAUGAG X CGAA AAUUUUCC	762	GGAAAATT A TTCAGGGC	2007
4432	CUGCCCUG CUGAUGAG X CGAA AUAAUUUU	763	AAAATTAT T CAGGGCAG	2008
4433	GCUGCCCU CUGAUGAG X CGAA AAUAAUUU	764	AAATTATT C AGGGCAGC	2009
4443	AGCAAAAU CUGAUGAG X CGAA AGCUGCCC	765	GGGCAGCT A ATTTTGCT	2010
4446	AAAAGCAA CUGAUGAG X CGAA AUUAGCUG	766	CAGCTAAT T TTGCTTTT	2011
4447	UAAAAGCA CUGAUGAG X CGAA AAUUAGCU	767	AGCTAATT T TGCTTTTA	2012
4448	GUAAAAGC CUGAUGAG X CGAA AAAUUAGC	768	GCTAATTT T GCTTTTAC	2013
4452	UUUGGUAA CUGAUGAG X CGAA AGCAAAAU	769	ATTTTGCT T TTACCAAA	2014
4453	UUUUGGUA CUGAUGAG X CGAA AAGCAAAA	770	TTTTGCTT T TACCAAAA	2015
4454	AUUUUGGU CUGAUGAG X CGAA AAAGCAAA	771	TTTGCTTT T ACCAAAAT	2016

4455	UAUUUUGG CUGAUGAG X CGAA AAAAGCAA	772	TTGCTTTT A CCAAAATA	2017
4463	ACUACUGA CUGAUGAG X CGAA AUUUUGGU	773	ACCAAAAT A TCAGTAGT	2018
4465	UUACUACU CUGAUGAG X CGAA AUAUUUUG	774	CAAAATAT C AGTAGTAA	2019
4469	AAUAUUAC CUGAUGAG X CGAA ACUGAUAU	775	ATATCAGT A GTAATATT	2020
4472	AAAAAUAU CUGAUGAG X CGAA ACUACUGA	776	TCAGTAGT A ATATTTTT	2021
4475	UCCAAAAA CUGAUGAG X CGAA AUUACUAC	777	GTAGTAAT A TTTTTGGA	2022
4477	UGUCCAAA CUGAUGAG X CGAA AUAUUACU	778	AGTAATAT T TTTGGACA	2023
4478	CUGUCCAA CUGAUGAG X CGAA AAUAUUAC	779	GTAATATT T TTGGACAG	2024
4479	ACUGUCCA CUGAUGAG X CGAA AAAUAUUA	780	TAATATTT T TGGACAGT	2025
4480	UACUGUCC CUGAUGAG X CGAA AAAAUAUU	781	AATATTTT T GGACAGTA	2026
4488	CCAUUAGC CUGAUGAG X CGAA ACUGUCCA	782	TGGACAGT A GCTAATGG	2027
4492	UGACCCAU CUGAUGAG X CGAA AGCUACUG	783	CAGTAGCT A ATGGGTCA	2028
4499	AACCCACU CUGAUGAG X CGAA ACCCAUUA	784	TAATGGGT C AGTGGGTT	2029
4507	UUAAAAAG CUGAUGAG X CGAA ACCCACUG	785	CAGTGGGT T CTTTTTAA	2030
4508	AUUAAAAA CUGAUGAG X CGAA AACCCACU	786	AGTGGGTT C TTTTTAAT	2031
4510	ACAUUAAA CUGAUGAG X CGAA AGAACCCA	787	TGGGTTCT T TTTAATGT	2032
4511	AACAUUAA CUGAUGAG X CGAA AAGAACCC	788	GGGTTCTT T TTAATGTT	2033
4512	AAACAUUA CUGAUGAG X CGAA AAAGAACC	789	GGTTCTTT T TAATGTTT	2034
4513	UAAACAUU CUGAUGAG X CGAA AAAAGAAC	790	GTTCTTTT T AATGTTTA	2035
4514	AUAAACAU CUGAUGAG X CGAA AAAAAGAA	791	TTCTTTTT A ATGTTTAT	2036
4519	UAAGUAUA CUGAUGAG X CGAA ACAUUAAA	792	TTTAATGT T TATACTTA	2037
4520	CUAAGUAU CUGAUGAG X CGAA AACAUUAA	793	TTAATGTT T ATACTTAG	2038
4521	UCUAAGUA CUGAUGAG X CGAA AAACAUUA	794	TAATGTTT A TACTTAGA	2039
4523	AAUCUAAG CUGAUGAG X CGAA AUAAACAU	795	ATGTTTAT A CTTAGATT	2040
4526	GAAAAUCU CUGAUGAG X CGAA AGUAUAAA	796	TTTATACT T AGATTTTC	2041
4527	AGAAAAUC CUGAUGAG X CGAA AAGUAUAA	797	TTATACTT A GATTTTCT	2042
4531	UAAAAGAA CUGAUGAG X CGAA AUCUAAGU	798	ACTTAGAT T TTCTTTTA	2043
4532	UUAAAAGA CUGAUGAG X CGAA AAUCUAAG	799	CTTAGATT T TCTTTTAA	2044
4533	UUUAAAAG CUGAUGAG X CGAA AAAUCUAA	800	TTAGATTT T CTTTTAAA	2045
4534	UUUUAAAA CUGAUGAG X CGAA AAAAUCUA	801	TAGATTTT C TTTTAAAA	2046
4536	UUUUUUAA CUGAUGAG X CGAA AGAAAAUC	802	GATTTTCT T TTAAAAAA	2047

4537	UUUUUUUA CUGAUGAG X CGAA AAGAAAAU	803	ATTTTCTT T TAAAAAAA	2048
4538	AUUUUUUU CUGAUGAG X CGAA AAAGAAAA	804	TTTTCTTT T AAAAAAAT	2049
4539	AAUUUUUU CUGAUGAG X CGAA AAAAGAAA	805	TTTCTTTT A AAAAAATT	2050
4547	UUUAUUUU CUGAUGAG X CGAA AUUUUUUU	806	AAAAAAAT T AAAATAAA	2051
4548	UUUUAUUU CUGAUGAG X CGAA AAUUUUUU	807	AAAAAATT A AAATAAAA	2052
4553	UUUUGUUU CUGAUGAG X CGAA AUUUUAAU	808	ATTAAAAT A AAACAAAA	2053
4567	GUCCUAGA CUGAUGAG X CGAA AUUUUUUU	809	AAAAAAAT T TCTAGGAC	2054
4568	AGUCCUAG CUGAUGAG X CGAA AAUUUUUU	810	AAAAAATT T CTAGGACT	2055
4569	UAGUCCUA CUGAUGAG X CGAA AAAUUUUU	811	AAAAATTT C TAGGACTA	2056
4571	UCUAGUCC CUGAUGAG X CGAA AGAAAUUU	812	AAATTTCT A GGACTAGA	2057
4577	ACAUCGUC CUGAUGAG X CGAA AGUCCUAG	813	CTAGGACT A GACGATGT	2058
4586	GCUGGUAU CUGAUGAG X CGAA ACAUCGUC	814	GACGATGT A ATACCAGC	2059
4589	UUAGCUGG CUGAUGAG X CGAA AUUACAUC	815	GATGTAAT A CCAGCTAA	2060
4596	UUUGGCUU CUGAUGAG X CGAA AGCUGGUA	816	TACCAGCT A AAGCCAAA	2061
4609	CACUGUAU CUGAUGAG X CGAA AUUGUUUG	817	CAAACAAT T ATACAGTG	2062
4610	CCACUGUA CUGAUGAG X CGAA AAUUGUUU	818	AAACAATT A TACAGTGG	2063
4612	UUCCACUG CUGAUGAG X CGAA AUAAUUGU	819	ACAATTAT A CAGTGGAA	2064
4624	UAAUGUAA CUGAUGAG X CGAA ACCUUCCA	820	TGGAAGGT T TTACATTA	2065
4625	AUAAUGUA CUGAUGAG X CGAA AACCUUCC	821	GGAAGGTT T TACATTAT	2066
4626	AAUAAUGU CUGAUGAG X CGAA AAACCUUC	822	GAAGGTTT T ACATTATT	2067
4627	GAAUAAUG CUGAUGAG X CGAA AAAACCUU	823	AAGGTTTT A CATTATTC	2068
4631	GGAUGAAU CUGAUGAG X CGAA AUGUAAAA	824	TTTTACAT T ATTCATCC	2069
4632	UGGAUGAA CUGAUGAG X CGAA AAUGUAAA	825	TTTACATT A TTCATCCA	2070
4634	AUUGGAUG CUGAUGAG X CGAA AUAAUGUA	826	TACATTAT T CATCCAAT	2071
4635	CAUUGGAU CUGAUGAG X CGAA AAUAAUGU	827	ACATTATT C ATCCAATG	2072
4638	ACACAUUG CUGAUGAG X CGAA AUGAAUAA	828	TTATTCAT C CAATGTGT	2073
4647	UGAAUAGA CUGAUGAG X CGAA ACACAUUG	829	CAATGTGT T TCTATTCA	2074
4648	AUGAAUAG CUGAUGAG X CGAA AACACAUU	830	AATGTGTT T CTATTCAT	2075
4649	CAUGAAUA CUGAUGAG X CGAA AAACACAU	831	ATGTGTTT C TATTCATG	2076
4651	AACAUGAA CUGAUGAG X CGAA AGAAACAC	832	GTGTTTCT A TTCATGTT	2077
4653	UUAACAUG CUGAUGAG X CGAA AUAGAAAC	833	GTTTCTAT T CATGTTAA	2078

4654	CUUAACAU CUGAUGAG X CGAA AAUAGAAA	834	TTTCTATT C ATGTTAAG	2079
4659	AGUAUCUU CUGAUGAG X CGAA ACAUGAAU	835	ATTCATGT T AAGATACT	2080
4660	UAGUAUCU CUGAUGAG X CGAA AACAUGAA	836	TTCATGTT A AGATACTA	2081
4665	UGUAGUAG CUGAUGAG X CGAA AUCUUAAC	837	GTTAAGAT A CTACTACA	2082
4668	AAAUGUAG CUGAUGAG X CGAA AGUAUCUU	838	AAGATACT A CTACATTT	2083
4671	UUCAAAUG CUGAUGAG X CGAA AGUAGUAU	839	ATACTACT A CATTTGAA	2084
4675	CCACUUCA CUGAUGAG X CGAA AUGUAGUA	840	TACTACAT T TGAAGTGG	2085
4676	CCCACUUC CUGAUGAG X CGAA AAUGUAGU	841	ACTACATT T GAAGTGGG	2086
4695	AAUCAUCU CUGAUGAG X CGAA AUGUUCUC	842	GAGAACAT C AGATGATT	2087
4703	AACAUUUC CUGAUGAG X CGAA AUCAUCUG	843	CAGATGAT T GAAATGTT	2088
4711	CCUGGGCG CUGAUGAG X CGAA ACAUUUCA	844	TGAAATGT T CGCCCAGG	2089
4712	CCCUGGGC CUGAUGAG X CGAA AACAUUUC	845	GAAATGTT C GCCCAGGG	2090
4723	UUGCUGGA CUGAUGAG X CGAA ACCCCUGG	846	CCAGGGGT C TCCAGCAA	2091
4725	AGUUGCUG CUGAUGAG X CGAA AGACCCCU	847	AGGGGTCT C CAGCAACT	2092
4734	GAUUUCCA CUGAUGAG X CGAA AGUUGCUG	848	CAGCAACT T TGGAAATC	2093
4735	AGAUUUCC CUGAUGAG X CGAA AAGUUGCU	849	AGCAACTT T GGAAATCT	2094
4742	UACAAAGA CUGAUGAG X CGAA AUUUCCAA	850	TTGGAAAT C TCTTTGTA	2095
4744	AAUACAAA CUGAUGAG X CGAA AGAUUUCC	851	GGAAATCT C TTTGTATT	2096
4746	AAAAUACA CUGAUGAG X CGAA AGAGAUUU	852	AAATCTCT T TGTATTTT	2097
4747	AAAAAUAC CUGAUGAG X CGAA AAGAGAUU	853	AATCTCTT T GTATTTTT	2098
4750	AGUAAAAA CUGAUGAG X CGAA ACAAAGAG	854	CTCTTTGT A TTTTTACT	2099
4752	CAAGUAAA CUGAUGAG X CGAA AUACAAAG	855	CTTTGTAT T TTTACTTG	2100
4753	UCAAGUAA CUGAUGAG X CGAA AAUACAAA	856	TTTGTATT T TTACTTGA	2101
4754	UUCAAGUA CUGAUGAG X CGAA AAAUACAA	857	TTGTATTT T TACTTGAA	2102
4755	CUUCAAGU CUGAUGAG X CGAA AAAAUACA	858	TGTATTTT T ACTTGAAG	2103
4756	ACUUCAAG CUGAUGAG X CGAA AAAAAUAC	859	GTATTTTT A CTTGAAGT	2104
4759	GGCACUUC CUGAUGAG X CGAA AGUAAAAA	860	TTTTTACT T GAAGTGCC	2105
4771	CUGUCCAU CUGAUGAG X CGAA AGUGGCAC	861	GTGCCACT A ATGGACAG	2106
4785	CCAGAAAA CUGAUGAG X CGAA AUCUGCUG	862	CAGCAGAT A TTTTCTGG	2107
4787	AGCCAGAA CUGAUGAG X CGAA AUAUCUGC	863	GCAGATAT T TTCTGGCT	2108
4788	CAGCCAGA CUGAUGAG X CGAA AAUAUCUG	864	CAGATATT T TCTGGCTG	2109

4789	UCAGCCAG CUGAUGAG X CGAA AAAUAUCU	865	AGATATTT T CTGGCTGA	2110
4790	AUCAGCCA CUGAUGAG X CGAA AAAAUAUC	866	GATATTTT C TGGCTGAT	2111
4801	CCAAUACC CUGAUGAG X CGAA ACAUCAGC	867	GCTGATGT T GGTATTGG	2112
4805	ACACCCAA CUGAUGAG X CGAA ACCAACAU	868	ATGTTGGT A TTGGGTGT	2113
4807	CUACACCC CUGAUGAG X CGAA AUACCAAC	869	GTTGGTAT T GGGTGTAG	2114
4814	CAUGUUCC CUGAUGAG X CGAA ACACCCAA	870	TTGGGTGT A GGAACATG	2115
4825	UUUUUUUA CUGAUGAG X CGAA AUCAUGUU	871	AACATGAT T TAAAAAAA	2116
4826	UUUUUUUU CUGAUGAG X CGAA AAUCAUGU	872	ACATGATT T AAAAAAAA	2117
4827	UUUUUUUU CUGAUGAG X CGAA AAAUCAUG	873	CATGATTT A AAAAAAAA	2118
4839	AGAGGCAA CUGAUGAG X CGAA AGUUUUUU	874	AAAAAACT C TTGCCTCT	2119
4841	GCAGAGGC CUGAUGAG X CGAA AGAGUUUU	875	AAAACTCT T GCCTCTGC	2120
4846	GGAAAGCA CUGAUGAG X CGAA AGGCAAGA	876	TCTTGCCT C TGCTTTCC	2121
4851	GUGGGGGA CUGAUGAG X CGAA AGCAGAGG	877	CCTCTGCT T TCCCCCAC	2122
4852	AGUGGGGG CUGAUGAG X CGAA AAGCAGAG	878	CTCTGCTT T CCCCCACT	2123
4853	GAGUGGGG CUGAUGAG X CGAA AAAGCAGA	879	TCTGCTTT C CCCCACTC	2124
4861	UUGCCUCA CUGAUGAG X CGAA AGUGGGGG	880	CCCCCACT C TGAGGCAA	2125
4872	UACAUUUU CUGAUGAG X CGAA ACUUGCCU	881	AGGCAAGT T AAAATGTA	2126
4873	UUACAUUU CUGAUGAG X CGAA AACUUGCC	882	GGCAAGTT A AAATGTAA	2127
4880	ACAUCUUU CUGAUGAG X CGAA ACAUUUUA	883	TAAAATGT A AAAGATGT	2128
4892	CCCAGAUA CUGAUGAG X CGAA AUCACAUC	884	GATGTGAT T TATCTGGG	2129
4893	CCCCAGAU CUGAUGAG X CGAA AAUCACAU	885	ATGTGATT T ATCTGGGG	2130
4894	CCCCCAGA CUGAUGAG X CGAA AAAUCACA	886	TGTGATTT A TCTGGGGG	2131
4896	GCCCCCCA CUGAUGAG X CGAA AUAAAUCA	887	TGATTTAT C TGGGGGGC	2132
4906	CCAUACCU CUGAUGAG X CGAA AGCCCCCC	888	GGGGGGCT C AGGTATGG	2133
4911	CCCCACCA CUGAUGAG X CGAA ACCUGAGC	889	GCTCAGGT A TGGTGGGG	2134
4928	GAUUCCUG CUGAUGAG X CGAA AUCCACUU	890	AAGTGGAT T CAGGAATC	2135
4929	AGAUUCCU CUGAUGAG X CGAA AAUCCACU	891	AGTGGATT C AGGAATCT	2136
4936	AUUCCCCA CUGAUGAG X CGAA AUUCCUGA	892	TCAGGAAT C TGGGGAAT	2137
4952	UCUUAAUA CUGAUGAG X CGAA AUUUGCCA	893	TGGCAAAT A TATTAAGA	2138
4954	CUUCUUAA CUGAUGAG X CGAA AUAUUUGC	894	GCAAATAT A TTAAGAAG	2139
4956	CUCUUCUU CUGAUGAG X CGAA AUAUAUUU	895	AAATATAT T AAGAAGAG	2140

4957	ACUCUUCU CUGAUGAG X CGAA AAUAUAUU	896	AATATATT A AGAAGAGT	2141
4966	ACUUUCAA CUGAUGAG X CGAA ACUCUUCU	897	AGAAGAGT A TTGAAAGT	2142
4968	AUACUUUC CUGAUGAG X CGAA AUACUCUU	898	AAGAGTAT T GAAAGTAT	2143
4975	CCUCCAAA CUGAUGAG X CGAA ACUUUCAA	899	TTGAAAGT A TTTGGAGG	2144
4977	UUCCUCCA CUGAUGAG X CGAA AUACUUUC	900	GAAAGTAT T TGGAGGAA	2145
4978	UUUCCUCC CUGAUGAG X CGAA AAUACUUU	901	AAAGTATT T GGAGGAAA	2146
4992	CCAGAAUU CUGAUGAG X CGAA ACCAUUUU	902	AAAATGGT T AATTCTGG	2147
4993	CCCAGAAU CUGAUGAG X CGAA AACCAUUU	903	AAATGGTT A ATTCTGGG	2148
4996	ACACCCAG CUGAUGAG X CGAA AUUAACCA	904	TGGTTAAT T CTGGGTGT	2149
4997	CACACCCA CUGAUGAG X CGAA AAUUAACC	905	GGTTAATT C TGGGTGTG	2150
5015	CUCUACUG CUGAUGAG X CGAA ACCUUGGU	906	ACCAAGGT T CAGTAGAG	2151
5016	ACUCUACU CUGAUGAG X CGAA AACCUUGG	907	CCAAGGTT C AGTAGAGT	2152
5020	GUGGACUC CUGAUGAG X CGAA ACUGAACC	908	GGTTCAGT A GAGTCCAC	2153
5025	CAGAAGUG CUGAUGAG X CGAA ACUCUACU	909	AGTAGAGT C CACTTCTG	2154
5030	CAGGGCAG CUGAUGAG X CGAA AGUGGACU	910	AGTCCACT T CTGCCCTG	2155
5031	CCAGGGCA CUGAUGAG X CGAA AAGUGGAC	911	GTCCACTT C TGCCCTGG	2156
5051	AGCUAGUU CUGAUGAG X CGAA AUUUGUGG	912	CCACAAAT C AACTAGCT	2157
5056	AAUGGAGC CUGAUGAG X CGAA AGUUGAUU	913	AATCAACT A GCTCCATT	2158
5060	UGUAAAUG CUGAUGAG X CGAA AGCUAGUU	914	AACTAGCT C CATTTACA	2159
5064	UGGCUGUA CUGAUGAG X CGAA AUGGAGCU	915	AGCTCCAT T TACAGCCA	2160
5065	AUGGCUGU CUGAUGAG X CGAA AAUGGAGC	916	GCTCCATT T ACAGCCAT	2161
5066	AAUGGCUG CUGAUGAG X CGAA AAAUGGAG	917	CTCCATTT A CAGCCATT	2162
5074	AUUUUAGA CUGAUGAG X CGAA AUGGCUGU	918	ACAGCCAT T TCTAAAAT	2163
5075	CAUUUUAG CUGAUGAG X CGAA AAUGGCUG	919	CAGCCATT T CTAAAATG	2164
5076	CCAUUUUA CUGAUGAG X CGAA AAAUGGCU	920	AGCCATTT C TAAAATGG	2165
5078	UGCCAUUU CUGAUGAG X CGAA AGAAAUGG	921	CCATTTCT A AAATGGCA	2166
5090	UAGAACUG CUGAUGAG X CGAA AGCUGCCA	922	TGGCAGCT T CAGTTCTA	2167
5091	CUAGAACU CUGAUGAG X CGAA AAGCUGCC	923	GGCAGCTT C AGTTCTAG	2168
5095	UUCUCUAG CUGAUGAG X CGAA ACUGAAGC	924	GCTTCAGT T CTAGAGAA	2169
5096	CUUCUCUA CUGAUGAG X CGAA AACUGAAG	925	CTTCAGTT C TAGAGAAG	2170
5098	UUCUUCUC CUGAUGAG X CGAA AGAACUGA	926	TCAGTTCT A GAGAAGAA	2171

5117	UUACUGCU CUGAUGAG X CGAA AUGUUGUU	927	AACAACAT C AGCAGTAA	2172
5124	AUGGACUU CUGAUGAG X CGAA ACUGCUGA	928	TCAGCAGT A AAGTCCAT	2173
5129	AUUCCAUG CUGAUGAG X CGAA ACUUUACU	929	AGTAAAGT C CATGGAAT	2174
5138	CCACUAGC CUGAUGAG X CGAA AUUCCAUG	930	CATGGAAT A GCTAGTGG	2175
5142	CAGACCAC CUGAUGAG X CGAA AGCUAUUC	931	GAATAGCT A GTGGTCTG	2176
5148	GAAACACA CUGAUGAG X CGAA ACCACUAG	932	CTAGTGGT C TGTGTTTC	2177
5154	CGAAAAGA CUGAUGAG X CGAA ACACAGAC	933	GTCTGTGT T TCTTTTCG	2178
5155	GCGAAAAG CUGAUGAG X CGAA AACACAGA	934	TCTGTGTT T CTTTTCGC	2179
5156	GGCGAAAA CUGAUGAG X CGAA AAACACAG	935	CTGTGTTT C TTTTCGCC	2180
5158	AUGGCGAA CUGAUGAG X CGAA AGAAACAC	936	GTGTTTCT T TTCGCCAT	2181
5159	AAUGGCGA CUGAUGAG X CGAA AAGAAACA	937	TGTTTCTT T TCGCCATT	2182
5160	CAAUGGCG CUGAUGAG X CGAA AAAGAAAC	938	GTTTCTTT T CGCCATTG	2183
5161	GCAAUGGC CUGAUGAG X CGAA AAAAGAAA	939	TTTCTTTT C GCCATTGC	2184
5167	AGCUAGGC CUGAUGAG X CGAA AUGGCGAA	940	TTCGCCAT T GCCTAGCT	2185
5172	CGGCAAGC CUGAUGAG X CGAA AGGCAAUG	941	CATTGCCT A GCTTGCCG	2186
5176	AUUACGGC CUGAUGAG X CGAA AGCUAGGC	942	GCCTAGCT T GCCGTAAT	2187
5182	AGAAUCAU CUGAUGAG X CGAA ACGGCAAG	943	CTTGCCGT A ATGATTCT	2188
5188	CAUUAUAG CUGAUGAG X CGAA AUCAUUAC	944	GTAATGAT T CTATAATG	2189
5189	GCAUUAUA CUGAUGAG X CGAA AAUCAUUA	945	TAATGATT C TATAATGC	2190
5191	UGGCAUUA CUGAUGAG X CGAA AGAAUCAU	946	ATGATTCT A TAATGCCA	2191
5193	GAUGGCAU CUGAUGAG X CGAA AUAGAAUC	947	GATTCTAT A ATGCCATC	2192
5201	UGCUGCAU CUGAUGAG X CGAA AUGGCAUU	948	AATGCCAT C ATGCAGCA	2193
5212	CCUCUCAU CUGAUGAG X CGAA AUUGCUGC	949	GCAGCAAT T ATGAGAGG	2194
5213	GCCUCUCA CUGAUGAG X CGAA AAUUGCUG	950	CAGCAATT A TGAGAGGC	2195
5223	GGAUGACC CUGAUGAG X CGAA AGCCUCUC	951	GAGAGGCT A GGTCATCC	2196
5227	CUUUGGAU CUGAUGAG X CGAA ACCUAGCC	952	GGCTAGGT C ATCCAAAG	2197
5230	UCUCUUUG CUGAUGAG X CGAA AUGACCUA	953	TAGGTCAT C CAAAGAGA	2198
5246	UACAUUGA CUGAUGAG X CGAA AGGGUCUU	954	AAGACCCT A TCAATGTA	2199
5248	CCUACAUU CUGAUGAG X CGAA AUAGGGUC	955	GACCCTAT C AATGTAGG	2200
5254	UUGCAACC CUGAUGAG X CGAA ACAUUGAU	956	ATCAATGT A GGTTGCAA	2201
5258	GAUUUUGC CUGAUGAG X CGAA ACCUACAU	957	ATGTAGGT T GCAAAATC	2202

5266	AGGGGUUA CUGAUGAG X CGAA AUUUUGCA	958	TGCAAAAT C TAACCCCT	2203
5268	UUAGGGGU CUGAUGAG X CGAA AGAUUUUG	959	CAAAATCT A ACCCCTAA	2204
5275	CACUUCCU CUGAUGAG X CGAA AGGGGUUA	960	TAACCCCT A AGGAAGTG	2205
5288	AAAUCAAA CUGAUGAG X CGAA ACUGCACU	961	AGTGCAGT C TTTGATTT	2206
5290	UCAAAUCA CUGAUGAG X CGAA AGACUGCA	962	TGCAGTCT T TGATTTGA	2207
5291	AUCAAAUC CUGAUGAG X CGAA AAGACUGC	963	GCAGTCTT T GATTTGAT	2208
5295	GGAAAUCA CUGAUGAG X CGAA AUCAAAGA	964	TCTTTGAT T TGATTTCC	2209
5296	GGGAAAUC CUGAUGAG X CGAA AAUCAAAG	965	CTTTGATT T GATTTCCC	2210
5300	ACUAGGGA CUGAUGAG X CGAA AUCAAAUC	966	GATTTGAT T TCCCTAGT	2211
5301	UACUAGGG CUGAUGAG X CGAA AAUCAAAU	967	ATTTGATT T CCCTAGTA	2212
5302	UUACUAGG CUGAUGAG X CGAA AAAUCAAA	968	TTTGATTT C CCTAGTAA	2213
5306	AAGGUUAC CUGAUGAG X CGAA AGGGAAAU	969	ATTTCCCT A GTAACCTT	2214
5309	UGCAAGGU CUGAUGAG X CGAA ACUAGGGA	970	TCCCTAGT A ACCTTGCA	2215
5314	AUAUCUGC CUGAUGAG X CGAA AGGUUACU	971	AGTAACCT T GCAGATAT	2216
5321	GUUAAACA CUGAUGAG X CGAA AUCUGCAA	972	TTGCAGAT A TGTTTAAC	2217
5325	CUUGGUUA CUGAUGAG X CGAA ACAUAUCU	973	AGATATGT T TAACCAAG	2218
5326	GCUUGGUU CUGAUGAG X CGAA AACAUAUC	974	GATATGTT T AACCAAGC	2219
5327	GGCUUGGU CUGAUGAG X CGAA AAACAUAU	975	ATATGTTT A ACCAAGCC	2220
5338	GCAUGGGC CUGAUGAG X CGAA AUGGCUUG	976	CAAGCCAT A GCCCATGC	2221
5349	GCCCUCAA CUGAUGAG X CGAA AGGCAUGG	977	CCATGCCT T TTGAGGGC	2222
5350	AGCCCUCA CUGAUGAG X CGAA AAGGCAUG	978	CATGCCTT T TGAGGGCT	2223
5351	CAGCCCUC CUGAUGAG X CGAA AAAGGCAU	979	ATGCCTTT T GAGGGCTG	2224
5367	AAGUCCCU CUGAUGAG X CGAA AUUUGUUC	980	GAACAAAT A AGGGACTT	2225
5375	UUAUCAGU CUGAUGAG X CGAA AGUCCCUU	981	AAGGGACT T ACTGATAA	2226
5376	AUUAUCAG CUGAUGAG X CGAA AAGUCCCU	982	AGGGACTT A CTGATAAT	2227
5382	AAGUAAAU CUGAUGAG X CGAA AUCAGUAA	983	TTACTGAT A ATTTACTT	2228
5385	CAAAAGUA CUGAUGAG X CGAA AUUAUCAG	984	CTGATAAT T TACTTTTG	2229
5386	UCAAAAGU CUGAUGAG X CGAA AAUUAUCA	985	TGATAATT T ACTTTTGA	2230
5387	AUCAAAAG CUGAUGAG X CGAA AAAUUAUC	986	GATAATTT A CTTTTGAT	2231
5390	GUGAUCAA CUGAUGAG X CGAA AGUAAAUU	987	AATTTACT T TTGATCAC	2232
5391	UGUGAUCA CUGAUGAG X CGAA AAGUAAAU	988	ATTTACTT T TGATCACA	2233

5392	AUGUGAUC CUGAUGAG X CGAA AAAGUAAA	989	TTTACTTT T GATCACAT	2234
5396	CUUAAUGU CUGAUGAG X CGAA AUCAAAAG	990	CTTTTGAT C ACATTAAG	2235
5401	AACACCUU CUGAUGAG X CGAA AUGUGAUC	991	GATCACAT T AAGGTGTT	2236
5402	GAACACCU CUGAUGAG X CGAA AAUGUGAU	992	ATCACATT A AGGTGTTC	2237
5409	AAGGUGAG CUGAUGAG X CGAA ACACCUUA	993	TAAGGTGT T CTCACCTT	2238
5410	CAAGGUGA CUGAUGAG X CGAA AACACCUU	994	AAGGTGTT C TCACCTTG	2239
5412	UUCAAGGU CUGAUGAG X CGAA AGAACACC	995	GGTGTTCT C ACCTTGAA	2240
5417	AAGAUUUC CUGAUGAG X CGAA AGGUGAGA	996	TCTCACCT T GAAATCTT	2241
5423	GUGUAUAA CUGAUGAG X CGAA AUUUCAAG	997	CTTGAAAT C TTATACAC	2242
5425	CAGUGUAU CUGAUGAG X CGAA AGAUUUCA	998	TGAAATCT T ATACACTG	2243
5426	UCAGUGUA CUGAUGAG X CGAA AAGAUUUC	999	GAAATCTT A TACACTGA	2244
5428	UUUCAGUG CUGAUGAG X CGAA AUAAGAUU	1000	AATCTTAT A CACTGAAA	2245
5444	CCUAAAUC CUGAUGAG X CGAA AUGGCCAU	1001	ATGGCCAT T GATTTAGG	2246
5448	GUGGCCUA CUGAUGAG X CGAA AUCAAUGG	1002	CCATTGAT T TAGGCCAC	2247
5449	AGUGGCCU CUGAUGAG X CGAA AAUCAAUG	1003	CATTGATT T AGGCCACT	2248
5450	CAGUGGCC CUGAUGAG X CGAA AAAUCAAU	1004	ATTGATTT A GGCCACTG	2249
5462	AGUACUCU CUGAUGAG X CGAA AGCCAGUG	1005	CACTGGCT T AGAGTACT	2250
5463	GAGUACUC CUGAUGAG X CGAA AAGCCAGU	1006	ACTGGCTT A GAGTACTC	2251
5468	GGAAGGAG CUGAUGAG X CGAA ACUCUAAG	1007	CTTAGAGT A CTCCTTCC	2252
5471	AGGGGAAG CUGAUGAG X CGAA AGUACUCU	1008	AGAGTACT C CTTCCCCT	2253
5474	UGCAGGGG CUGAUGAG X CGAA AGGAGUAC	1009	GTACTCCT T CCCCTGCA	2254
5475	AUGCAGGG CUGAUGAG X CGAA AAGGAGUA	1010	TACTCCTT C CCCTGCAT	2255
5493	GUAUUUGU CUGAUGAG X CGAA AUCAGUGU	1011	ACACTGAT T ACAAATAC	2256
5494	AGUAUUUG CUGAUGAG X CGAA AAUCAGUG	1012	CACTGATT A CAAATACT	2257
5500	UAGGAAAG CUGAUGAG X CGAA AUUUGUAA	1013	TTACAAAT A CTTTCCTA	2258
5503	GAAUAGGA CUGAUGAG X CGAA AGUAUUUG	1014	CAAATACT T TCCTATTC	2259
5504	UGAAUAGG CUGAUGAG X CGAA AAGUAUUU	1015	AAATACTT T CCTATTCA	2260
5505	AUGAAUAG CUGAUGAG X CGAA AAAGUAUU	1016	AATACTTT C CTATTCAT	2261
5508	AGUAUGAA CUGAUGAG X CGAA AGGAAAGU	1017	ACTTTCCT A TTCATACT	2262
5510	AAAGUAUG CUGAUGAG X CGAA AUAGGAAA	1018	TTTCCTAT T CATACTTT	2263
5511	GAAAGUAU CUGAUGAG X CGAA AAUAGGAA	1019	TTCCTATT C ATACTTTC	2264

5514	UUGGAAAG CUGAUGAG X CGAA AUGAAUAG	1020	CTATTCAT A CTTTCCAA	2265
5517	UAAUUGGA CUGAUGAG X CGAA AGUAUGAA	1021	TTCATACT T TCCAATTA	2266
5518	AUAAUUGG CUGAUGAG X CGAA AAGUAUGA	1022	TCATACTT T CCAATTAT	2267
5519	CAUAAUUG CUGAUGAG X CGAA AAAGUAUG	1023	CATACTTT C CAATTATG	2268
5524	CAUCUCAU CUGAUGAG X CGAA AUUGGAAA	1024	TTTCCAAT T ATGAGATG	2269
5525	CCAUCUCA CUGAUGAG X CGAA AAUUGGAA	1025	TTCCAATT A TGAGATGG	2270
5543	ACUCCCAG CUGAUGAG X CGAA ACCCACAG	1026	CTGTGGGT A CTGGGAGT	2271
5555	GUGUUAGU CUGAUGAG X CGAA AUCACUCC	1027	GGAGTGAT C ACTAACAC	2272
5559	UAUGGUGU CUGAUGAG X CGAA AGUGAUCA	1028	TGATCACT A ACACCATA	2273
5567	GACAUUAC CUGAUGAG X CGAA AUGGUGUU	1029	AACACCAT A GTAATGTC	2274
5570	UUAGACAU CUGAUGAG X CGAA ACUAUGGU	1030	ACCATAGT A ATGTCTAA	2275
5575	GAAUAUUA CUGAUGAG X CGAA ACAUUACU	1031	AGTAATGT C TAATATTC	2276
5577	GUGAAUAU CUGAUGAG X CGAA AGACAUUA	1032	TAATGTCT A ATATTCAC	2277
5580	CCUGUGAA CUGAUGAG X CGAA AUUAGACA	1033	TGTCTAAT A TTCACAGG	2278
5582	UGCCUGUG CUGAUGAG X CGAA AUAUUAGA	1034	TCTAATAT T CACAGGCA	2279
5583	CUGCCUGU CUGAUGAG X CGAA AAUAUUAG	1035	CTAATATT C ACAGGCAG	2280
5594	CCCAAGCA CUGAUGAG X CGAA AUCUGCCU	1036	AGGCAGAT C TGCTTGGG	2281
5599	GCUUCCCC CUGAUGAG X CGAA AGCAGAUC	1037	GATCTGCT T GGGGAAGC	2282
5609	CACAUAAC CUGAUGAG X CGAA AGCUUCCC	1038	GGGAAGCT A GTTATGTG	2283
5612	UUUCACAU CUGAUGAG X CGAA ACUAGCUU	1039	AAGCTAGT T ATGTGAAA	2284
5613	CUUUCACA CUGAUGAG X CGAA AACUAGCU	1040	AGCTAGTT A TGTGAAAG	2285
5628	UAUGACUU CUGAUGAG X CGAA AUUUGCCU	1041	AGGCAAAT A AAGTCATA	2286
5633	UACUGUAU CUGAUGAG X CGAA ACUUUAUU	1042	AATAAAGT C ATACAGTA	2287
5636	AGCUACUG CUGAUGAG X CGAA AUGACUUU	1043	AAAGTCAT A CAGTAGCT	2288
5641	UUUUGAGC CUGAUGAG X CGAA ACUGUAUG	1044	CATACAGT A GCTCAAAA	2289
5645	UGCCUUUU CUGAUGAG X CGAA AGCUACUG	1045	CAGTAGCT C AAAAGGCA	2290
5659	AAGAGAAU CUGAUGAG X CGAA AUGGUUGC	1046	GCAACCAT A ATTCTCTT	2291
5662	CCAAAGAG CUGAUGAG X CGAA AUUAUGGU	1047	ACCATAAT T CTCTTTGG	2292
5663	ACCAAAGA CUGAUGAG X CGAA AAUUAUGG	1048	CCATAATT C TCTTTGGT	2293
5665	GCACCAAA CUGAUGAG X CGAA AGAAUUAU	1049	ATAATTCT C TTTGGTGC	2294
5667	UUGCACCA CUGAUGAG X CGAA AGAGAAUU	1050	AATTCTCT T TGGTGCAA	2295

5668	CUUGCACC CUGAUGAG X CGAA AAGAGAAU	1051	ATTCTCTT T GGTGCAAG	2296
5678	GCUCCCAA CUGAUGAG X CGAA ACUUGCAC	1052	GTGCAAGT C TTGGGAGC	2297
5680	ACGCUCCC CUGAUGAG X CGAA AGACUUGC	1053	GCAAGTCT T GGGAGCGT	2298
5692	GUAAUCUA CUGAUGAG X CGAA AUCACGCU	1054	AGCGTGAT C TAGATTAC	2299
5694	GUGUAAUC CUGAUGAG X CGAA AGAUCACG	1055	CGTGATCT A GATTACAC	2300
5698	UGCAGUGU CUGAUGAG X CGAA AUCUAGAU	1056	ATCTAGAT T ACACTGCA	2301
5699	GUGCAGUG CUGAUGAG X CGAA AAUCUAGA	1057	TCTAGATT A CACTGCAC	2302
5711	AACUUGGG CUGAUGAG X CGAA AUGGUGCA	1058	TGCACCAT T CCCAAGTT	2303
5712	UAACUUGG CUGAUGAG X CGAA AAUGGUGC	1059	GCACCATT C CCAAGTTA	2304
5719	AGGGGAUU CUGAUGAG X CGAA ACUUGGGA	1060	TCCCAAGT T AATCCCCT	2305
5720	CAGGGGAU CUGAUGAG X CGAA AACUUGGG	1061	CCCAAGTT A ATCCCCTG	2306
5723	UUUCAGGG CUGAUGAG X CGAA AUUAACUU	1062	AAGTTAAT C CCCTGAAA	2307
5735	UUGAGAGU CUGAUGAG X CGAA AGUUUUCA	1063	TGAAAACT T ACTCTCAA	2308
5736	GUUGAGAG CUGAUGAG X CGAA AAGUUUUC	1064	GAAAACTT A CTCTCAAC	2309
5739	CCAGUUGA CUGAUGAG X CGAA AGUAAGUU	1065	AACTTACT C TCAACTGG	2310
5741	CUCCAGUU CUGAUGAG X CGAA AGAGUAAG	1066	CTTACTCT C AACTGGAG	2311
5760	UGGGACCA CUGAUGAG X CGAA AGUUCAUU	1067	AATGAACT T TGGTCCCA	2312
5761	UUGGGACC CUGAUGAG X CGAA AAGUUCAU	1068	ATGAACTT T GGTCCCAA	2313
5765	AUAUUUGG CUGAUGAG X CGAA ACCAAAGU	1069	ACTTTGGT C CCAAATAT	2314
5772	AAGAUGGA CUGAUGAG X CGAA AUUUGGGA	1070	TCCCAAAT A TCCATCTT	2315
5774	AAAAGAUG CUGAUGAG X CGAA AUAUUUGG	1071	CCAAATAT C CATCTTTT	2316
5778	ACUGAAAA CUGAUGAG X CGAA AUGGAUAU	1072	ATATCCAT C TTTTCAGT	2317
5780	CUACUGAA CUGAUGAG X CGAA AGAUGGAU	1073	ATCCATCT T TTCAGTAG	2318
5781	GCUACUGA CUGAUGAG X CGAA AAGAUGGA	1074	TCCATCTT T TCAGTAGC	2319
5782	CGCUACUG CUGAUGAG X CGAA AAAGAUGG	1075	CCATCTTT T CAGTAGCG	2320
5783	ACGCUACU CUGAUGAG X CGAA AAAAGAUG	1076	CATCTTTT C AGTAGCGT	2321
5787	AUUAACGC CUGAUGAG X CGAA ACUGAAAA	1077	TTTTCAGT A GCGTTAAT	2322
5792	GCAUAAUU CUGAUGAG X CGAA ACGCUACU	1078	AGTAGCGT T AATTATGC	2323
5793	AGCAUAAU CUGAUGAG X CGAA AACGCUAC	1079	GTAGCGTT A ATTATGCT	2324
5796	CAGAGCAU CUGAUGAG X CGAA AUUAACGC	1080	GCGTTAAT T ATGCTCTG	2325
5797	ACAGAGCA CUGAUGAG X CGAA AAUUAACG	1081	CGTTAATT A TGCTCTGT	2326

5802	UGGAAACA CUGAUGAG X CGAA AGCAUAAU	1082	ATTATGCT C TGTTTCCA	2327
5806	CAGUUGGA CUGAUGAG X CGAA ACAGAGCA	1083	TGCTCTGT T TCCAACTG	2328
5807	GCAGUUGG CUGAUGAG X CGAA AACAGAGC	1084	GCTCTGTT T CCAACTGC	2329
5808	UGCAGUUG CUGAUGAG X CGAA AAACAGAG	1085	CTCTGTTT C CAACTGCA	2330
5818	GGAAAGGA CUGAUGAG X CGAA AUGCAGUU	1086	AACTGCAT T TCCTTTCC	2331
5819	UGGAAAGG CUGAUGAG X CGAA AAUGCAGU	1087	ACTGCATT T CCTTTCCA	2332
5820	UUGGAAAG CUGAUGAG X CGAA AAAUGCAG	1088	CTGCATTT C CTTTCCAA	2333
5823	CAAUUGGA CUGAUGAG X CGAA AGGAAAUG	1089	CATTTCCT T TCCAATTG	2334
5824	UCAAUUGG CUGAUGAG X CGAA AAGGAAAU	1090	ATTTCCTT T CCAATTGA	2335
5825	UUCAAUUG CUGAUGAG X CGAA AAAGGAAA	1091	TTTCCTTT C CAATTGAA	2336
5830	UUUAAUUC CUGAUGAG X CGAA AUUGGAAA	1092	TTTCCAAT T GAATTAAA	2337
5835	CACACUUU CUGAUGAG X CGAA AUUCAAUU	1093	AATTGAAT T AAAGTGTG	2338
5836	CCACACUU CUGAUGAG X CGAA AAUUCAAU	1094	ATTGAATT A AAGTGTGG	2339
5848	CUAAAAAC CUGAUGAG X CGAA AGGCCACA	1095	TGTGGCCT C GTTTTTAG	2340
5851	UGACUAAA CUGAUGAG X CGAA ACGAGGCC	1096	GGCCTCGT T TTTAGTCA	2341
5852	AUGACUAA CUGAUGAG X CGAA AACGAGGC	1097	GCCTCGTT T TTAGTCAT	2342
5853	AAUGACUA CUGAUGAG X CGAA AAACGAGG	1098	CCTCGTTT T TAGTCATT	2343
5854	AAAUGACU CUGAUGAG X CGAA AAAACGAG	1099	CTCGTTTT T AGTCATTT	2344
5855	UAAAUGAC CUGAUGAG X CGAA AAAAACGA	1100	TCGTTTTT A GTCATTTA	2345
5858	UUUUAAAU CUGAUGAG X CGAA ACUAAAAA	1101	TTTTTAGT C ATTTAAAA	2346
5861	CAAUUUUA CUGAUGAG X CGAA AUGACUAA	1102	TTAGTCAT T TAAAATTG	2347
5862	ACAAUUUU CUGAUGAG X CGAA AAUGACUA	1103	TAGTCATT T AAAATTGT	2348
5863	AACAAUUU CUGAUGAG X CGAA AAAUGACU	1104	AGTCATTT A AAATTGTT	2349
5868	UAGAAAAC CUGAUGAG X CGAA AUUUUAAA	1105	TTTAAAAT T GTTTTCTA	2350
5871	ACUUAGAA CUGAUGAG X CGAA ACAAUUUU	1106	AAAATTGT T TTCTAAGT	2351
5872	UACUUAGA CUGAUGAG X CGAA AACAAUUU	1107	AAATTGTT T TCTAAGTA	2352
5873	UUACUUAG CUGAUGAG X CGAA AAACAAUU	1108	AATTGTTT T CTAAGTAA	2353
5874	AUUACUUA CUGAUGAG X CGAA AAAACAAU	1109	ATTGTTTT C TAAGTAAT	2354
5876	CAAUUACU CUGAUGAG X CGAA AGAAAACA	1110	TGTTTTCT A AGTAATTG	2355
5880	GCAGCAAU CUGAUGAG X CGAA ACUUAGAA	1111	TTCTAAGT A ATTGCTGC	2356
5883	GAGGCAGC CUGAUGAG X CGAA AUUACUUA	1112	TAAGTAAT T GCTGCCTC	2357

5891	CCAUAAUA CUGAUGAG X CGAA AGGCAGCA	1113	TGCTGCCT C TATTATGG	2358
5893	UGCCAUAA CUGAUGAG X CGAA AGAGGCAG	1114	CTGCCTCT A TTATGGCA	2359
5895	AGUGCCAU CUGAUGAG X CGAA AUAGAGGC	1115	GCCTCTAT T ATGGCACT	2360
5896	AAGUGCCA CUGAUGAG X CGAA AAUAGAGG	1116	CCTCTATT A TGGCACTT	2361
5904	CAAAAUUG CUGAUGAG X CGAA AGUGCCAU	1117	ATGGCACT T CAATTTTG	2362
5905	GCAAAAUU CUGAUGAG X CGAA AAGUGCCA	1118	TGGCACTT C AATTTTGC	2363
5909	CAGUGCAA CUGAUGAG X CGAA AUUGAAGU	1119	ACTTCAAT T TTGCACTG	2364
5910	ACAGUGCA CUGAUGAG X CGAA AAUUGAAG	1120	CTTCAATT T TGCACTGT	2365
5911	GACAGUGC CUGAUGAG X CGAA AAAUUGAA	1121	TTCAATTT T GCACTGTC	2366
5919	UCUCAAAA CUGAUGAG X CGAA ACAGUGCA	1122	TGCACTGT C TTTTGAGA	2367
5921	AAUCUCAA CUGAUGAG X CGAA AGACAGUG	1123	CACTGTCT T TTGAGATT	2368
5922	GAAUCUCA CUGAUGAG X CGAA AAGACAGU	1124	ACTGTCTT T TGAGATTC	2369
5923	UGAAUCUC CUGAUGAG X CGAA AAAGACAG	1125	CTGTCTTT T GAGATTCA	2370
5929	UUUUCUUG CUGAUGAG X CGAA AUCUCAAA	1126	TTTGAGAT T CAAGAAAA	2371
5930	UUUUUCUU CUGAUGAG X CGAA AAUCUCAA	1127	TTGAGATT C AAGAAAAA	2372
5940	UGAAUAGA CUGAUGAG X CGAA AUUUUUCU	1128	AGAAAAAT T TCTATTCA	2373
5941	AUGAAUAG CUGAUGAG X CGAA AAUUUUUC	1129	GAAAAATT T CTATTCAT	2374
5942	AAUGAAUA CUGAUGAG X CGAA AAAUUUUU	1130	AAAAATTT C TATTCATT	2375
5944	AAAAUGAA CUGAUGAG X CGAA AGAAAUUU	1131	AAATTTCT A TTCATTTT	2376
5946	AAAAAAUG CUGAUGAG X CGAA AUAGAAAU	1132	ATTTCTAT T CATTTTTT	2377
5947	AAAAAAAU CUGAUGAG X CGAA AAUAGAAA	1133	TTTCTATT C ATTTTTTT	2378
5950	UGCAAAAA CUGAUGAG X CGAA AUGAAUAG	1134	CTATTCAT T TTTTTGCA	2379
5951	AUGCAAAA CUGAUGAG X CGAA AAUGAAUA	1135	TATTCATT T TTTTGCAT	2380
5952	GAUGCAAA CUGAUGAG X CGAA AAAUGAAU	1136	ATTCATTT T TTTGCATC	2381
5953	GGAUGCAA CUGAUGAG X CGAA AAAAUGAA	1137	TTCATTTT T TTGCATCC	2382
5954	UGGAUGCA CUGAUGAG X CGAA AAAAAUGA	1138	TCATTTTT T TGCATCCA	2383
5955	UUGGAUGC CUGAUGAG X CGAA AAAAAAUG	1139	CATTTTTT T GCATCCAA	2384
5960	CACAAUUG CUGAUGAG X CGAA AUGCAAAA	1140	TTTTGCAT C CAATTGTG	2385
5965	UCAGGCAC CUGAUGAG X CGAA AUUGGAUG	1141	CATCCAAT T GTGCCTGA	2386
5977	UAUUUUAA CUGAUGAG X CGAA AGUUCAGG	1142	CCTGAACT T TTAAAATA	2387
5978	AUAUUUUA CUGAUGAG X CGAA AAGUUCAG	1143	CTGAACTT T TAAAATAT	2388

2226	GCAGGA AGAA GAAU ACCAGAGAAACA X GUACAUUACCUGGUA	2551	ATTC TGTC TCCTGC	2664
2301	ACUAAG AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	2552	GCTC AGTT CTTAGT	2665
2322	ACAGAA AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	2553	CTTC TGTC TTCTGT	2666
2329	GUUCCC AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	2554	CTTC TGTT GGGAAC	2667
2373	AAAGAG AGAA GUUA ACCAGAGAAACA X GUACAUUACCUGGUA	2555	TAAC AGCT CTCTTT	2668
2429	GAGUUC AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	2556	TCAC AGCT GAACTC	2669
2439	CCCAUA AGAA GAGU ACCAGAGAAACA X GUACAUUACCUGGUA	2557	ACTC AGTC TATGGG	2670
2768	UAGGGG AGAA GCCU ACCAGAGAAACA X GUACAUUACCUGGUA	2558	AGGC AGAT CCCCTA	2671
2812	CUCUGA AGAA GCAG ACCAGAGAAACA X GUACAUUACCUGGUA	2559	CTGC AGAT TCAGAG	2672
2835	GCCAGA AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	2560	GCTC TGCC TCTGGC	2673
2944	ACAAAA AGAA GGAA ACCAGAGAAACA X GUACAUUACCUGGUA	2561	TTCC TGAT TTTTGT	2674
3009	UCCUGA AGAA GACC ACCAGAGAAACA X GUACAUUACCUGGUA	2562	GGTC AGCT TCAGGA	2675
3021	CACUGG AGAA GGUC ACCAGAGAAACA X GUACAUUACCUGGUA	2563	GACC TGTT CCAGTG	2676
3083	ACAGUG AGAA GUUC ACCAGAGAAACA X GUACAUUACCUGGUA	2564	GAAC TGTT CACTGT	2677
3242	GCUCAG AGAA GUAU ACCAGAGAAACA X GUACAUUACCUGGUA	2565	ATAC AGTT CTGAGC	2678
3258	GAGCAA AGAA GGCU ACCAGAGAAACA X GUACAUUACCUGGUA	2566	AGCC AGAC TTGCTC	2679
3312	UGCGGG AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	2567	TTGC AGAC CCCGCA	2680
3360	AAUAAG AGAA GGAC ACCAGAGAAACA X GUACAUUACCUGGUA	2568	GTCC AGCT CTTATT	2681
3402	CUUGAC AGAA GCUU ACCAGAGAAACA X GUACAUUACCUGGUA	2569	AAGC AGCT GTCAAG	2682
3420	GAACAC AGAA GUCU ACCAGAGAAACA X GUACAUUACCUGGUA	2570	AGAC AGCT GTGTTC	2683
3475	GACAGC AGAA GUCC ACCAGAGAAACA X GUACAUUACCUGGUA	2571	GGAC CGTT GCTGTC	2684

3496	GCCCCA AGAA GCCU ACCAGAGAAACA X GUACAUUACCUGGUA	2572	AGGC TGAC TGGGGC	2685
3512	UACGUA AGAA GACC ACCAGAGAAACA X GUACAUUACCUGGUA	2573	GGTC AGAT TACGTA	2686
3595	GAACGG AGAA GGGG ACCAGAGAAACA X GUACAUUACCUGGUA	2574	CCCC CGCC CCGTTC	2687
3600	GUAGGG AGAA GGGC ACCAGAGAAACA X GUACAUUACCUGGUA	2575	GCCC CGTT CCCTAC	2688
3610	AGUGGA AGAA GUAG ACCAGAGAAACA X GUACAUUACCUGGUA	2576	CTAC CGCC TCCACT	2689
3626	GAAAUG AGAA GGCA ACCAGAGAAACA X GUACAUUACCUGGUA	2577	TGCC AGCT CATTTC	2690
3693	AGGGAA AGAA GCCC ACCAGAGAAACA X GUACAUUACCUGGUA	2578	GGGC AGCC TTCCCT	2691
3848	AGCCCG AGAA GCUA ACCAGAGAAACA X GUACAUUACCUGGUA	2579	TAGC TGCT CGGGCT	2692
3902	UGGACA AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	2580	TTTC TGAT TGTCCA	2693
4047	UAAACA AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	2581	TTGC TGTT TGTTTA	2694
4157	AUCCAG AGAA GAAU ACCAGAGAAACA X GUACAUUACCUGGUA	2582	ATTC TGTT CTGGAT	2695
4359	AUAGGC AGAA GGAU ACCAGAGAAACA X GUACAUUACCUGGUA	2583	ATCC AGAT GCCTAT	2696
4696	UCAAUC AGAA GAUG ACCAGAGAAACA X GUACAUUACCUGGUA	2584	CATC AGAT GATTGA	2697
4795	ACCAAC AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	2585	TGGC TGAT GTTGGT	2698
4847	GGGGAA AGAA GAGG ACCAGAGAAACA X GUACAUUACCUGGUA	2586	CCTC TGCT TTCCCC	2699
5032	CUCCAG AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	2587	CTTC TGCC CTGGAG	2700
5086	AACUGA AGAA GCCA ACCAGAGAAACA X GUACAUUACCUGGUA	2588	TGGC AGCT TCAGTT	2701
5092	CUCUAG AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	2589	CTTC AGTT CTAGAG	2702
5285	AUCAAA AGAA GCAC ACCAGAGAAACA X GUACAUUACCUGGUA	2590	GTGC AGTC TTTGAT	2703
5489	UUUGUA AGAA GUGU ACCAGAGAAACA X GUACAUUACCUGGUA	2591	ACAC TGAT TACAAA	2704
5590	AAGCAG AGAA GCCU ACCAGAGAAACA X GUACAUUACCUGGUA	2592	AGGC AGAT CTGCTT	2705

5595	UCCCCA AGAA GAUC ACCAGAGAAACA X GUACAUUACCUGGUA	2593	GATC TGCT TGGGGA	2706
5803	GUUGGA AGAA GAGC ACCAGAGAAACA X GUACAUUACCUGGUA	2594	GCTC TGTT TCCAAC	2707
5886	AAUAGA AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	2595	TTGC TGCC TCTATT	2708
5916	UCAAAA AGAA GUGC ACCAGAGAAACA X GUACAUUACCUGGUA	2596	GCAC TGTC TTTTGA	2709
6087	AAAGGG AGAA GUGU ACCAGAGAAACA X GUACAUUACCUGGUA	2597	ACAC AGAC CCCTTT	2710
6154	AACAGA AGAA GGCA ACCAGAGAAACA X GUACAUUACCUGGUA	2598	TGCC AGTT TCTGTT	2711
6160	UGAGAG AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	2599	TTTC TGTT CTCTCA	2712
6284	GUAUGC AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	2600	TTGC CGAT GCATAC	2713
6300	AGUCAC AGAA GUAA ACCAGAGAAACA X GUACAUUACCUGGUA	2601	TTAC TGAT GTGACT	2714
6311	CGACAA AGAA GAGU ACCAGAGAAACA X GUACAUUACCUGGUA	2602	ACTC GGTT TTGTCG	2715
6322	AAGCAA AGAA GCGA ACCAGAGAAACA X GUACAUUACCUGGUA	2603	TCGC AGCT TTGCTT	2716

Table VI. Ribozymes for in vitro Cleavage

Seq. ID. No	Ribozyme Sequence	% CLEAVED ABOVE BACKGROUND 2 HOURS
2727	[$A_sT_sA_sG_sA_sT_sT_sT_s$] cUGAuGaggccgaaaggccGaa Aggcacac B	3.2
2728	[$G_sC_sG_sG_sA_sA_sC_sC_s$] cUGAuGaggccgaaaggccGaa Agaugaug B	11
2729	[$T_sT_sT_sC_sC_sG_sA_s$] cUGAuGaggccgaaaggccGaa Agacaca B	1
2730	[$A_sT_sT_sC_sC_s$TsGs] cUGAuGaggccgaaaggccGaa Auuccuu B	80.8

Table VII. Antisense Nucleic Acid Molecules Targeting c-raf

Seq. I.D. No.	Sequence
2731	$c_sg_sa_sauugC_sA_sT_sC_sC_sT_sG_sA_sA_sacag_sa_sa_sA$
2732	$g_su_sa_scctgA_sT_sT_sC^m{}_sG_sC_sT_sG_sT_sgacu_su_sc_sG$
2733	$g_sc_sa_sccagC_sA_sC_sA_sG_sA_sC_sT_sT_saccu_sg_sa_sT$
2734	$u_sa_sg_scagcC_sC_sT_sG_sA_sG_sC_sC_sT_suacc_su_sg_sG$
2735	$c_sa_sg_sgaucT_sG_sA_sA_sA_sC_sA_sA_sA_sgccc_sa_sa_sG$
2736	$u_sg_sc_scaucT_sT_sT_sA_sC^m{}_sG_sA_sA_sC_scaac_sc_sc_sA$
2737	$g_su_sg_sgtcaG_sC^m{}_sG_sT_sG_sC_sA_sA_sG_scauu_sg_sa_sT$
2738	$T_sC_sC_sC_sG_sC_sC_sT_sG_sT_sG_sA_sC_sA_sT_sG_sC_sA_sT_sT_s$
2739	$T_sC_sC_sG_sC_sC_sG_sT_sC_sT_sC_sA_sG_sA_sT_sC_sG_sA_sT_sT_s$
2740	$agucccgC_sC_sT_sG_sT_sG_sA_sC_sA_sugcauuc$
2741	$a_sg_su_scccgC_sC_sT_sG_sT_sG_sA_sC_sA_sugcau_su_sC_s$
2742	$a_sg_su_scccgC_sC_sT_sG_sT_sG_sA_sC_sA_sugcau_su_sc_s$
2743	iB $agucccgC_sC_sT_sG_sT_sG_sA_sC_sA_sugcauuc$ iB
2744	**$agucccg$**$C_sC_sT_sG_sT_sG_sA_sC_sA_s$**$ugcauuc$** iB
2745	$gauccgcC_sG_sT_sC_sT_sC_sA_sG_sA_sucgaucu$
2746	$g_sa_su_sccgcC_sG_sT_sC_sT_sC_sA_sG_sA_sucga_su_sc_su$
2747	iB $gauccgcC_sG_sT_sC_sT_sC_sA_sG_sA_sucgaucu$ iB
2748	**$gauccgc$**$C_sG_sT_sC_sT_sC_sA_sG_sA_s$**$ucgaucu$** iB

lower case = 2'-O-methyl nucleotides; UPPER Case = DNA; s = phosphorothioate linkage; m= 5 methyl C;iB=inverted abasic;**bold lower case**=2'-*O*-methylthiomethyl modified

Table VIII. Antisense Nucleic Acid Molecules Targeting Bcl-2 and K-ras

Seq. I.D. No.	Target	Sequence
2749	Bcl-2	$c_sc_sc_sa_sccgA_sA_sC_sT_sC_sA_sA_sA_sG_saaggscscsa$ iB
2750	Bcl-2	$a_sa_sg_sc_sga$ $cC_sT_sA_sA_sA_sG_sC_sA_sA_sccccsa_sg_sc$ iB
2751	Bcl-2	iB $cccaccgA_sA_s$ $C_sT_sC_s$ $A_sA_sA_sG_saaggcca$ iB
2752	Bcl-2	$iBaagcgacC_sT_s$ $A_sA_cA_s$ $G_sC_sA_s$ A_scc cca gc iB
2753	Bcl-2	$c_sc_sc_sa_sccgA_cA_s$ $C_sT_sC_s$ $A_sA_sA_sG_saa$ gg_sc_s c_sa iB
2754	k-ras (rat)	$c_sc_sa_sccag$ $C_sT_sC_sC_sA_sA_sC_s$ $tacc_sa_sc_sA$
2755	k-ras (rat)	$t_sg_sg_scaaa$ $T_sA_sC_sA_sC_sA_sA_s$ $agaa_sa_sg_sC$
2756	k-ras (rat)	$c_sc_sa_staac$ $T_sC_sC_sT_sT_sG_sC_s$ $taac_st_sc_sC$
2757	k-ras (rat)	$c_sa_sc_scctg$ $T_sC_sT_sT_sG_sT_sC_s$ $ttcg_sc_st_sG$
2758	Estrogen Receptor	$c_su_sg_sccaggu$$T_sG_sG_sT_sC_sA_sG_s$$uaagcc_sc_sa_su$
2759	Estrogen Receptor	$a_sg_su_suucaA_sT_sC_sT_sT_sC_sU_sA_sA_s$$auug_sg_sc_sa$
2760	Estrogen Receptor	$T_sG_sC_s^MC_s^MA_sG_sG_sT_sT_sG_sG_sT_sC_s^MA_sG_sT_sA_sA_sG_sC_s^MC_s^M$ C_s^MA
2761	Estrogen Receptor	$T_sC_s^MG_sC_s^MA_sT_sG_sT_sG_sG_sC_s^MT_sG_sA_sG_sG_sA_sT_sA_sC_s^MG_sC_s^MA_s$ C_s^M
2762	Estrogen Receptor	ugc cag gT_sT_s $G_sG_sT_s$ $C_sA_sG_s$ T_saa gcc ca
2763	Estrogen Receptor	ucg cga $uG_sT_sG_sC_sT_sG_sA_sG_sA_sua$ cgc ac
2764	Estrogen Receptor	$u_sg_sc_s$ cag gT_sT_s $G_sG_sT_s$ $C_sA_sG_s$ T_saa gc_sc_s c_sa
2765	Estrogen Receptor	$g_sa_su_s$ ccg $cC_sG_sT_sC_sT_sC_sA_sG_sA_suc$ ga_su_s c_su
2766	Estrogen Receptor	iB ugc cag gT_sT_s $G_sG_sT_s$ $C_sA_sG_s$ T_saa gcc ca iB
2767	Estrogen Receptor	iB ucg cga $uG_sT_sG_sC_sT_sG_sA_sG_sA_sua$ cgc ac iB
2768	Estrogen Receptor	ugc cag gT_sT_s $G_sG_sT_s$ $C_sA_sG_s$ T_saa gcc ca iB
2769	Estrogen Receptor	**ucg cga u** $G_sT_sG_sC_sT_sG_sA_sG_sA_s$ **ua cgc ac** iB

lower case = 2'-O-methyl nucleotides; UPPER Case = DNA; s = phosphorothioate linkage;
m= 5 methyl C; iB=inverted abasic; **bold lower case**=2'-*O*-methylthiomethyl modified

Claims

1. A nucleic acid molecule having the formula **I**:

wherein each of X represents independently a nucleotide which may be same or different;

$$5' \quad C\text{——}(X)_m\text{——}(Y)_n\text{——}(X)_o\text{——}C' \quad 3'$$

where m and o are integers independently greater than or equal to 5; $(X)_m$ and $(X)_o$ are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid molecule; Y represents independently a deoxyribonucleotide which may be same or different; $(Y)_n$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule; n is an integer greater than or equal to 4; ___represents a chemical linkage; each $(X)_m$, and $(X)_o$ comprise independently at least one phosphodiester linkage and one phosphorothioate linkage; $(Y)_n$ comprises a phosphorothioate linkage or a phosphorodithioate linkage or a 5'-thiophosphate linkage or a mixture thereof; and each C and C' independently represents a cap structure which may independently be present or absent.

2. A nucleic acid molecule having the formula **II**:

$$5' \quad C\text{——}(Y)_n\text{——}(X)_r\text{——}C' \quad 3'$$

wherein X represents a nucleotide which may be same or different; where r is an integer greater than or equal to 4; $(X)_r$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule; Y represents independently a deoxyribonucleotide which may be same or different; n is an integer greater than or equal to 4; $(Y)_n$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule_____ represents a chemical linkage; $(Y)_n$ comprises a phosphorothioate linkage or a phosphorodithioate linkage or a 5'-thiophosphate linkage or a mixture thereof; each $(X)_r$ comprises independently at least one phosphodiester linkage and one phosphorothioate linkage; and each C and C' independently represents a cap structure which may independently be present or absent.

3. A nucleic acid molecule having the formula **III**:

$$5'\ C\text{—}(X)_r\text{——}(Y)_n\text{——}C'\ 3'$$

wherein X represents a nucleotide which may be same or different; where r is an integer greater than or equal to 4; $(X)_r$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule; Y represents independently a deoxyribonucleotide which may be same or different ; n is an integer greater than or equal to 4; $(Y)_n$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule_____ represents a chemical linkage; $(Y)_n$ comprises a phosphorothioate linkage or a phosphorodithioate linkage or a mixture of phosphorothioate and phosphorodithioate linkages; each $(X)_r$ comprises independently at least one phosphodiester linkage and one phosphorothioate linkage; and each C and C' independently represents a cap structure which may independently be present or absent.

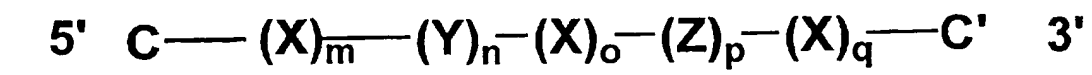
4. An enzymatic nucleic acid molecule having endonuclease activity of the formula IV:

$$5'\ C\text{——}(X)_m\text{——}(Z)_p\text{——}(X)_o\text{—}(Y)_n\text{——}(X)_q\text{—}C'\ 3'$$

wherein each of X represents independently a nucleotide which may be same or different; where m, o and q are integers independently greater than or equal to 5; $(X)_m$ and $(X)_o$ are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid molecule; $(X)_q$ is optionally able to interact with a target nucleic acid molecule;

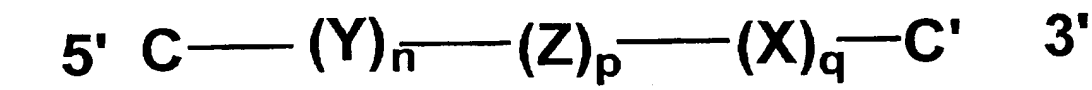
Y represents independently a deoxyribonucleotide which may be same or different; $(Y)_n$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule; n is an integer greater than or equal to 4; ____ represents a chemical linkage; each $(X)_m$, $(X)_o$ and $(X)_q$ comprise independently at least one phosphodiester linkage; $(Y)_n$ comprises a phosphorothioate linkage or a phosphorodithioate linkage or a 5'-thiophosphate linkage or a mixture thereof; Z represents an oligonucleotide able to facilitate the cleavage of the target nucleic acid molecule; p is of length greater than or equal to 4; and each C and C' independently represents a cap structure which may independently be present or absent.

5. An enzymatic nucleic acid molecule having endonuclease activity of the formula V:



wherein each of X represents independently a nucleotide which may be same or different; where m, o and q are integers independently greater than or equal to 5; $(X)_m$ and $(X)_o$ are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid molecule; $(X)_q$ is optionally able to interact with the target nucleic acid molecule; $(Y)_n$ represents independently a deoxyribonucleotide which may be same or different; $(Y)_n$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule; n is an integer greater than or equal to 4; ____ represents a chemical linkage; each $(X)_m$, $(X)_o$ and $(X)_q$ comprise independently at least one phosphodiester linkage; $(Y)_n$ comprises a phosphorothioate linkage or a phosphorodithioate linkage or a 5'-thiophosphate linkage or a mixture thereof; Z represents an oligonucleotide able to facilitate the cleavage of the target nucleic acid molecule; p is of length greater than or equal to 4; and each C and C' independently represents a cap structure which may independently be present or absent.

6. An enzymatic nucleic acid molecule having endonuclease activity of the formula VI:



wherein X represents independently a nucleotide which may be same or different; where q is an integer independently greater than or equal to 1; $(X)_q$ is optionally able to interact with a target nucleic acid molecule; Y represents independently a deoxyribonucleotide which may be same or different; $(Y)_n$ is an oligonucleotide which is of sufficient length to stably interact independently with a target nucleic acid molecule; n is an integer greater than or equal to 4; ___ represents a chemical linkage; $(Y)_n$ comprises a phosphorothioate linkage or a phosphorodithioate linkage or a 5'-thiophosphate linkage or a mixture thereof; Z represents an oligonucleotide able to facilitate the cleavage of the target nucleic acid

molecule; p is of length greater than or equal to 4; and each C and C' independently represents a cap structure which may independently be present or absent.

7. An enzymatic nucleic acid molecule having endonuclease activity of the formula VII:

$$5'\ C\text{---}(X)_q\text{---}(Z)_p\text{---}(Y)_n\text{---}C'\ \ 3'$$

wherein X represents independently a nucleotide which may be same or different; where q is an integer independently greater than or equal to 1; $(X)_q$ is optionally able to interact with a target nucleic acid molecule; Y represents independently a deoxyribonucleotide which may be same or different; $(Y)_n$ is an oligonucleotide which is of sufficient length to stably interact independently with the target nucleic acid molecule; n is an integer greater than or equal to 4; ___ represents a chemical linkage; $(Y)_n$ comprises a phosphorothioate linkage or a phosphorodithioate linkage or a 5'-S-phosphorothioate linkage or a 5'-S-phosphorodithioate linkage or a 3'-S-phosphorothioate linkage or a 3'-S-phosphorodithioate linkage or a mixture thereof; Z represents an oligonucleotide able to facilitate the cleavage of the target nucleic acid molecule; p is of length greater than or equal to 4; and each C and C' independently represents a cap structure which may independently be present or absent.

8. The nucleic acid molecule of any of claims 1-3, wherein each X, independently comprises a nucleotide modification selected from the group consisting of: 2'-*O*-methyl, 2'-*O*-allyl, 2'-*O*-methylthiomethyl, L-nucleotides; 2'-*C*-allyl; 1-5-Anhydrohexytol; 2,6-diaminopurine; 2'-fluoro; 2'-deoxy-2'-amino; 2'-(*N*-alanyl) amino; 2'-(*N*-phenylalanyl)amino; 2'-deoxy-2'-(*N*-β-alanyl) amino; 2'-deoxy-2'-(lysyl) amino; 2'-*O*-amino; 2'-Deoxy-2'-(*N*-histidyl) amino; 6-methyl uridine; 5-methyl cytidine; 2'-(*N*-β-carboxamidine-β-alanyl)amino-2'-deoxy-nucleotide; 2'-*O*-methylthioallyl; 2'-*O*-methylthioethyl; 2'-*O*-methylthiomethyl; 2'-*O*-methyl-3'-thiophosphate and xylofuranosyl.

9. The enzymatic nucleic acid molecule of any of claims 4-7, wherein each X, Z or both X and Z, independently comprises a nucleotide modification selected from the group consisting of: 2'-*O*-methyl, 2'-*O*-allyl, 2'-*O*-methylthiomethyl, L-nucleotides; 2'-*C*-allyl; 1-5-Anhydrohexytol; 2,6-diaminopurine; 2'-fluoro; 2'-deoxy-2'-amino; 2'-H; 2'-(*N*-

alanyl) amino; 2'-(*N*-phenylalanyl)amino; 2'-deoxy-2'-(*N*-β-alanyl) amino; 2'-deoxy-2'-(lysyl) amino; 2'-*O*-amino; 2'-Deoxy-2'-(*N*-histidyl) amino; 6-methyl uridine; 5-methyl cytidine; 2'-(*N*-β-carboxamidine-β-alanyl)amino-2'-deoxy-nucleotide; 2'-*O*-methylthioallyl; 2'-*O*-methylthioethyl; 2'-*O*-methylthiomethyl; 2'-*O*-methyl-3'-thiophosphate and xylofuranosyl.

10. The enzymatic nucleic acid molecule of any of claims 4-7, wherein, the Z in said nucleic acid molecule is the catalytic core.

11. The enzymatic nucleic acid molecule of any of claims 4-7, wherein said enzymatic nucleic acid is in a hammerhead ribozyme configuration.

12. The enzymatic nucleic acid molecule of any of claims 4-7, wherein said enzymatic nucleic acid is in a hairpin ribozyme configuration.

13. The enzymatic nucleic acid of any of claims 4-7, wherein said enzymatic nucleic acid is in a hepatitis delta virus, group I intron, VS RNA, group II intron, or RNase P RNA configuration.

14. A method of cleaving an RNA molecule comprising the step of, contacting the enzymatic nucleic acid molecule of any of claims 4-7, with the RNA molecule under conditions suitable for the cleavage of said RNA molecule by said enzymatic nucleic acid molecule.

15. The method of claim 14, wherein said cleavage is carried out in the presence of a divalent cation.

16. The method of claim 15, wherein said divalent cation is Mg^{2+}.

17. The nucleic acid molecules of any of claims 1-3, wherein said C', when present, is a cap selected from the group consisting of: inverted abasic residue; 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety;

3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; and methylphosphonate moiety.

18. The nucleic acid molecule of any of claim 1-3, wherein said nucleic acid molecule comprises a 3'-3' linked inverted ribose moiety at said 3' end.

19. The nucleic acid molecule of any of claims 1-3, wherein said nucleic acid molecule is an antisense nucleic acid molecule.

20. The nucleic acid molecule of claims 1-3 wherein said nucleic acid molecule is a 2-5A antisense chimera.

21. The nucleic acid molecule of any of claims 1-3 wherein said nucleic acid molecule is a triplex forming oligonucleotide.

22. A nucleic acid molecule comprising any of sequence defined as Seq. ID Nos. 1-30.

23. A mammalian cell including an enzymatic nucleic acid molecule of any of claims 4-7.

24. The mammalian cell of claim 23, wherein said mammalian cell is a human cell.

25. A method of modulating the expression of a gene in a cell comprising the step of administering to said cell a nucleic acid molecule of any of claims 1-3 under conditions suitable for the down regulation of said gene.

26. A method of modulating the expression of a gene in a cell comprising the step of administering to said cell an enzymatic nucleic acid molecule of any of claims 4-7 under conditions suitable for the down regulation of said gene.

27. The enzymatic nucleic acid molecule of any of claims 4-7, wherein said C', when present, is a cap selected from the group consisting of: inverted abasic residue; 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide,

carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; and methylphosphonate moiety.

28. The enzymatic nucleic acid molecule of any of claims 4-7, wherein said C, when present, is a cap selected from the group consisting of: 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moeity; 5'-5'-inverted abasic moeity; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moeities.

29. The nucleic acid molecules of any of claims 1-3, wherein said C, when present, is a cap selected from the group consisting of: 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moeity; 5'-5'-inverted abasic moeity; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties.

30. A mammalian cell including a nucleic acid molecule of any of claims 1-3.

31. The mammalian cell of claim 30, wherein said mammalian cell is a human cell.

32. The enzymatic nucleic acid molecule of any of claims 4-7, wherein said enzymatic nucleic acid molecule comprises a 3'-3' linked inverted ribose moiety at said 3' end.

33. The nucleic acid molecule of any of claims 1-3, wherein said $(X)_m$ and $(X)_o$ are symmetric in length.

34. The nucleic acid molecule of any of claims 1-3, wherein said $(X)_m$ and $(X)_o$ are asymmetric in length.

35. The enzymatic nucleic acid molecule of any of claims 4-5, wherein said $(X)_m$ and $(X)_o$ are symmetric in length.

36. The enzymatic nucleic acid molecule of any of claims 4-5, wherein said $(X)_m$ and $(X)_o$ are asymmetric in length.

37. The enzymatic nucleic acid molecule of claim 4, wherein the sum of said o, n and q is equal to said m.

38. The enzymatic nucleic acid molecule of claim 5, wherein the sum of said o, n and m is equal to said q.

39. The enzymatic nucleic acid molecule of claim 4, wherein the sum of said o, n and q is greater than said m.

40. The enzymatic nucleic acid molecule of claim 5, wherein the sum of said o, n and m is greater than said q.

41. The enzymatic nucleic acid molecule of claim 4, wherein the sum of said o, n and q is less than said m.

42. The enzymatic nucleic acid molecule of claim 5, wherein the sum of said o, n and m is less than said q.

43. An enzymatic nucleic acid molecule with RNA cleaving activity, wherein said enzymatic nucleic acid molecule modulates the expression of an estrogen receptor gene.

44. The enzymatic nucleic acid molecule of claim 43, wherein said enzymatic nucleic acid molecule is in a hammerhead configuration.

45. The enzymatic nucleic acid molecule of claim 44, wherein said enzymatic nucleic acid molecule comprises a stem II region of length greater than or equal to 2 base pairs.

46. The enzymatic nucleic acid molecule of claim 43, wherein said enzymatic nucleic acid molecule is in a hairpin configuration.

47. The enzymatic nucleic acid molecule of claim 43, wherein said enzymatic nucleic acid is in a hepatitis d virus, group I intron, group II intron, VS nucleic acid or RNase P nucleic acid configuration.

48. The enzymatic nucleic acid of claim 46, wherein said enzymatic nucleic acid molecule comprises a stem II region of length between three and seven base-pairs.

49. The enzymatic nucleic acid molecule of claim 43, wherein said nucleic acid comprises between 12 and 100 bases complementary to said RNA.

50. The enzymatic nucleic acid molecule of claim 43, wherein said nucleic acid comprises between 14 and 24 bases complementary to said mRNA.

51. The enzymatic nucleic acid molecule of claim 44, wherein said enzymatic nucleic acid molecule consists essentially of any sequence defined as Seq ID Nos 1-1245.

52. A mammalian cell including an enzymatic nucleic acid molecule of any of claim 43.

53. The mammalian cell of claim 52, wherein said mammalian cell is a human cell.

54. An expression vector comprising nucleic acid sequence encoding at least one enzymatic nucleic acid molecule of claim 43, in a manner which allows expression of that enzymatic nucleic acid molecule.

55. A mammalian cell including an expression vector of claim 54.

56. The mammalian cell of claim 13, wherein said mammalian cell is a human cell.

57. A method for treatment of cancer comprising the step of administering to a patient the enzymatic nucleic acid molecule of claim 43.

58. A method for treatment of cancer comprising the step of administering to a patient the expression vector of claim 54.

59. A method for treatment of cancer comprising the steps of: a) isolating cells from a patient; b) administering to said cells the enzymatic nucleic acid molecule of claim 43; and c) introducing said cells back into said patient.

60. A pharmaceutical composition comprising the enzymatic nucleic acid molecule of claim 43.

61. A method of treatment of a patient having a condition associated with the level of estrogen receptor, wherein said patient is administered the enzymatic nucleic acid molecule of claim 43.

62. A method of treatment of a patient having a condition associated with the level of estrogen receptor, comprising contacting cells of said patient with the nucleic acid molecule of claim 43, and further comprising the use of one or more drug therapies.

63. The enzymatic nucleic acid molecule of claim 44, wherein said nucleic acid molecule comprises at least five ribose residues, and wherein said nucleic acid comprises phosphorothioate linkages at at least three of the 5' terminal nucleotides, and wherein said nucleic acid comprises a 2'-*C*-allyl modification at position No. 4 of said nucleic acid, and wherein said nucleic acid comprises at least ten 2'-*O*-methyl modifications, and wherein said nucleic acid comprises a 3'- end modification.

64. The enzymatic nucleic acid of claim 63, wherein said nucleic acid comprises a 3'-3' linked inverted ribose moiety at said 3' end.

65. The enzymatic nucleic acid molecule of claim 44, wherein said nucleic acid molecule comprises at least five ribose residues, and wherein said nucleic acid molecule comprises phosphorothioate linkages at at least three of the 5' terminal nucleotides, and wherein said nucleic acid comprises a 2'-amino modification at position No. 4 and/or at position No. 7 of said nucleic acid molecule, wherein said nucleic acid molecule comprises at least ten 2'-*O*-methyl modifications, and wherein said nucleic acid comprises a 3'- end modification.

66. The enzymatic nucleic acid molecule of claim 44, wherein said nucleic acid molecule comprises at least five ribose residues, and wherein said nucleic acid molecule comprises phosphorothioate linkages at at least three of the 5' terminal nucleotides, and wherein said nucleic acid molecule comprises an abasic substitution at position No. 4 and/or at position No. 7 of said nucleic acid molecule, wherein said nucleic acid comprises at least ten 2'-*O*-methyl modifications, and wherein said nucleic acid molecule comprises a 3'-end modification.

67. The enzymatic nucleic acid molecule of claim 44, wherein said nucleic acid molecule comprises of at least five ribose residues, and wherein said nucleic acid comprises phosphorothioate linkages at at least three of the 5' terminal nucleotides, and wherein said nucleic acid molecule comprises a 6-methyl uridine substitution at position No. 4 and/or at position No. 7 of said nucleic acid molecule, wherein said nucleic acid molecule comprises at least ten 2'-*O*-methyl modifications, and wherein said nucleic acid molecule comprises a 3' end modification.

68. A method for modulating expression of estrogen receptor gene in a mammalian cell by administering to said cell the enzymatic nucleic acid molecule of claim 43.

69. A method of cleaving a separate RNA molecule comprising, contacting the enzymatic nucleic acid molecule of claim 43 with said separate RNA molecule under conditions suitable for the cleavage of said separate RNA molecule.

70. The method of claim 69, wherein said cleavage is carried out in the presence of a divalent cation.

71. The method of claim 70, wherein said divalent cation is Mg^{2+}.

72. The nucleic acid molecule of claim 43, wherein said nucleic acid is chemically synthesized.

73. The expression vector of claim 54, wherein said vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) a gene encoding at least one said nucleic acid molecule; and

wherein said gene is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

74. The expression vector of claim 54, wherein said vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an open reading frame;

d) a gene encoding at least one said nucleic acid molecule, wherein said gene is operably linked to the 3'-end of said open reading frame; and

wherein said gene is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

75. The expression vector of claim 54, wherein said vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an intron;

d) a gene encoding at least one said nucleic acid molecule; and

wherein said gene is operably linked to said initiation region, said intron and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

76. The expression vector of claim 54, wherein said vector comprises:

a) a transcription initiation region;

b) a transcription termination region;

c) an intron;

d) an open reading frame;

e) a gene encoding at least one said nucleic acid molecule, wherein said gene is operably linked to the 3'-end of said open reading frame; and

wherein said gene is operably linked to said initiation region, said intron, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

77. The enzymatic nucleic acid molecule of claim 44, wherein said enzymatic nucleic acid comprises sequences that are complementary to any of sequences defined as Seq ID Nos 1246-2490.

78. The enzymatic nucleic acid molecule of claim 46, wherein said enzymatic nucleic acid molecule consists essentially of any sequence defined as Seq ID Nos 2491-2603.

79. The enzymatic nucleic acid molecule of claim 46, wherein said enzymatic nucleic acid comprises sequences that are complementary to any of sequences defined as Seq ID Nos 2604-2716..

80. The enzymatic nucleic acid molecule of claim 43, wherein said enzymatic nucleic acid is a DNA enzyme.

81. The enzymatic nucleic acid molecule of claim 43, wherein said enzymatic nucleic acid comprises at least one 2'-sugar modification.

82. The enzymatic nucleic acid molecule of claim 43, wherein said enzymatic nucleic acid comprises at least one nucleic acid base modification.

83. The enzymatic nucleic acid molecule of claim 43, wherein said enzymatic nucleic acid comprises at least one phosphorothioate modification.

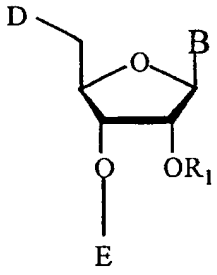
84. The enzymatic nucleic acid molecule of any of claims 4-7, wherein said enzymatic nucleic acid molecule comprises a 3'-3' linked inverted deoxyribose moiety at said 3' end.

85. The nucleic acid molecule of any of claims 1-3, wherein said enzymatic nucleic acid molecule comprises a 3'-3' linked inverted deoxyribose moiety at said 3' end.

86. The nucleic acid molecule of any of claims 1-3, wherein said enzymatic nucleic acid molecule comprises a 5'-5' linked inverted deoxyribose moiety at said 5' end.

87. The enzymatic nucleic acid molecule of any of claims 4-7, wherein said enzymatic nucleic acid molecule comprises a 5'-5' linked inverted deoxyribose moiety at said 5' end.

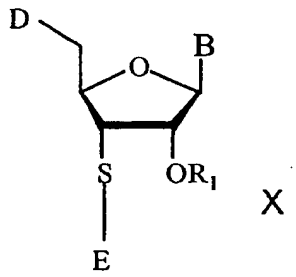
88. The nucleic acid molecule of any of claims 1-3, wherein each X, independently comprises a nucleotide modification having formula IX:



IX

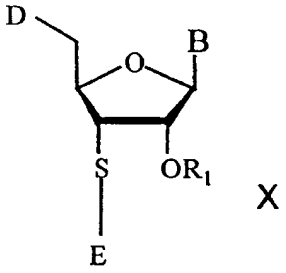
Wherein, each B is independently a modified or an unmodified nucleic acid base; R1 is independently an aklyl, an alkylthioalkyl, a fluoroalkyl or an alkylthiofluoroalkyl; E is independently a phosphorus-containing group; and D is independently an O, blocking group or a phosphorus-containing group.

89. The nucleic acid molecule of any of claims 1-3, wherein each X, independently comprises a nucleotide modification having formula X:



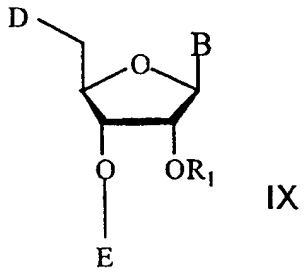
Wherein, each B is independently a modified or an unmodified nucleic acid base; R1 is independently an aklyl, an alkylthioalkyl, a fluoroalkyl or an alkylthiofluoroalkyl; E is independently a phosphorus-containing group; and D is independently an O, blocking group or a phosphorus-containing group.

90. The nucleic acid molecule of any of claims 4-7, wherein each X, Z or both X and Z, independently comprise a nucleotide modification having formula X:



Wherein, each B is independently a modified or an unmodified nucleic acid base; R1 is independently an aklyl, an alkylthioalkyl, a fluoroalkyl or an alkylthiofluoroalkyl; E is independently a phosphorus-containing group; and D is independently an O, blocking group or a phosphorus-containing group.

91. The nucleic acid molecule of any of claims 4-7, wherein each X, Z or both X and Z, independently comprises a nucleotide modification having formula IX:



IX

Wherein, each B is independently a modified or an unmodified nucleic acid base; R1 is independently an aklyl, an alkylthioalkyl, a fluoroalkyl or an alkylthiofluoroalkyl; E is independently a phosphorus-containing group; and D is independently an O, blocking group or a phosphorus-containing group.

92. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a phosphorothioate linkage.

93. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a phosphorodithioate linkage.

94. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a 5'-S-phosphorothioate linkage.

95. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ consists of phosphorothioate linkage at every position.

96. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ consists of phosphorodithioate linkage at every position.

97. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ consists of 5'-S-phosphorothioate linkage at every position.

98. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorothioate and phosphorodithioate linkages.

99. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorothioate and 5'-S-phosphorothioate linkages.

100. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorodithioate and 5'-S-phosphorothioate linkages.

101. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorothioate, phosphorodithioate and 5'-S-phosphorothioate linkages.

102. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorothioate and 5'-S-phosphorodithioate linkages.

103. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorodithioate and 5'-S-phosphorodithioate linkages.

104. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorothioate and 3'-S-phosphorothioate linkages.

105. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorodithioate and 3'-S-phosphorothioate linkages.

106. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorothioate and 3'-S-phosphorodithioate linkages.

107. The nucleic acid molecule of any of claims 1-3 and 4-7, wherein $(Y)_n$ comprises a combination of phosphorodithioate and 3'-S-phosphorodithioate linkages.

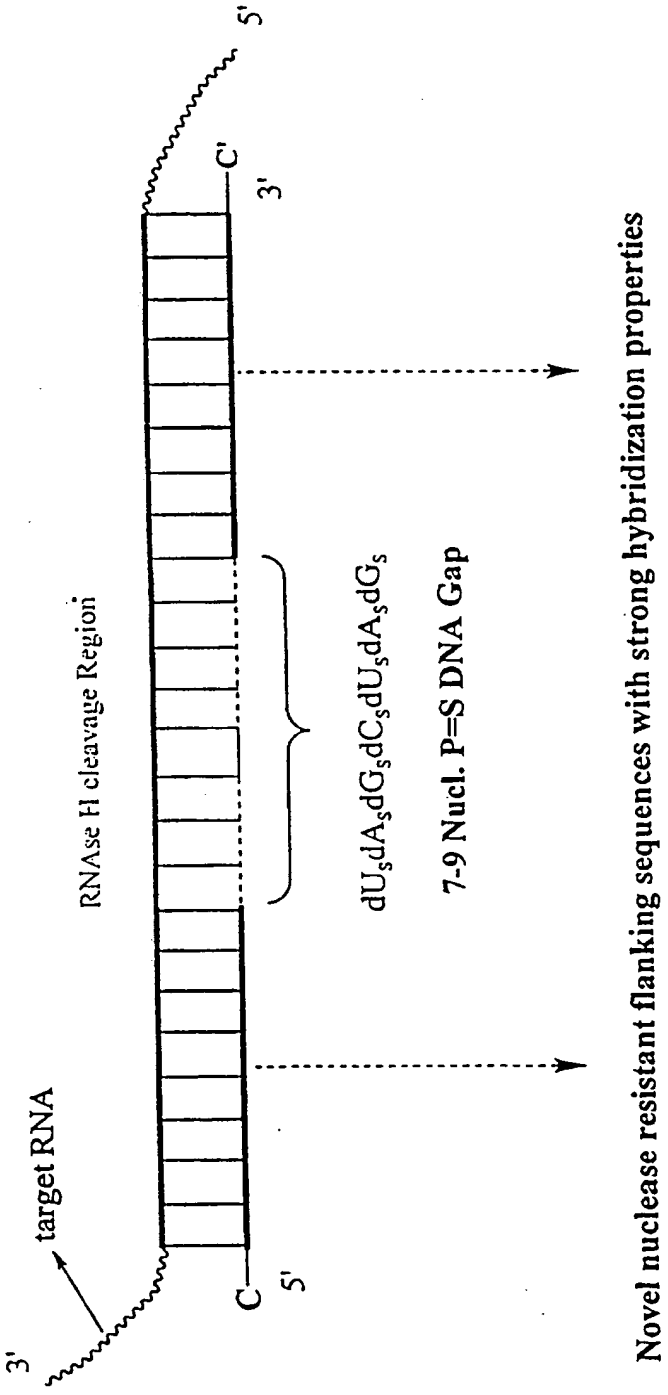

5'
C'
3'
RNAse H cleavage Region
$dU_sdA_sdG_sdC_sdC_sdU_sdA_sdG_s$
7-9 Nucl. P=S DNA Gap
Novel nuclease resistant flanking sequences with strong hybridization properties
target RNA
3'
C
5'

Fig. 1

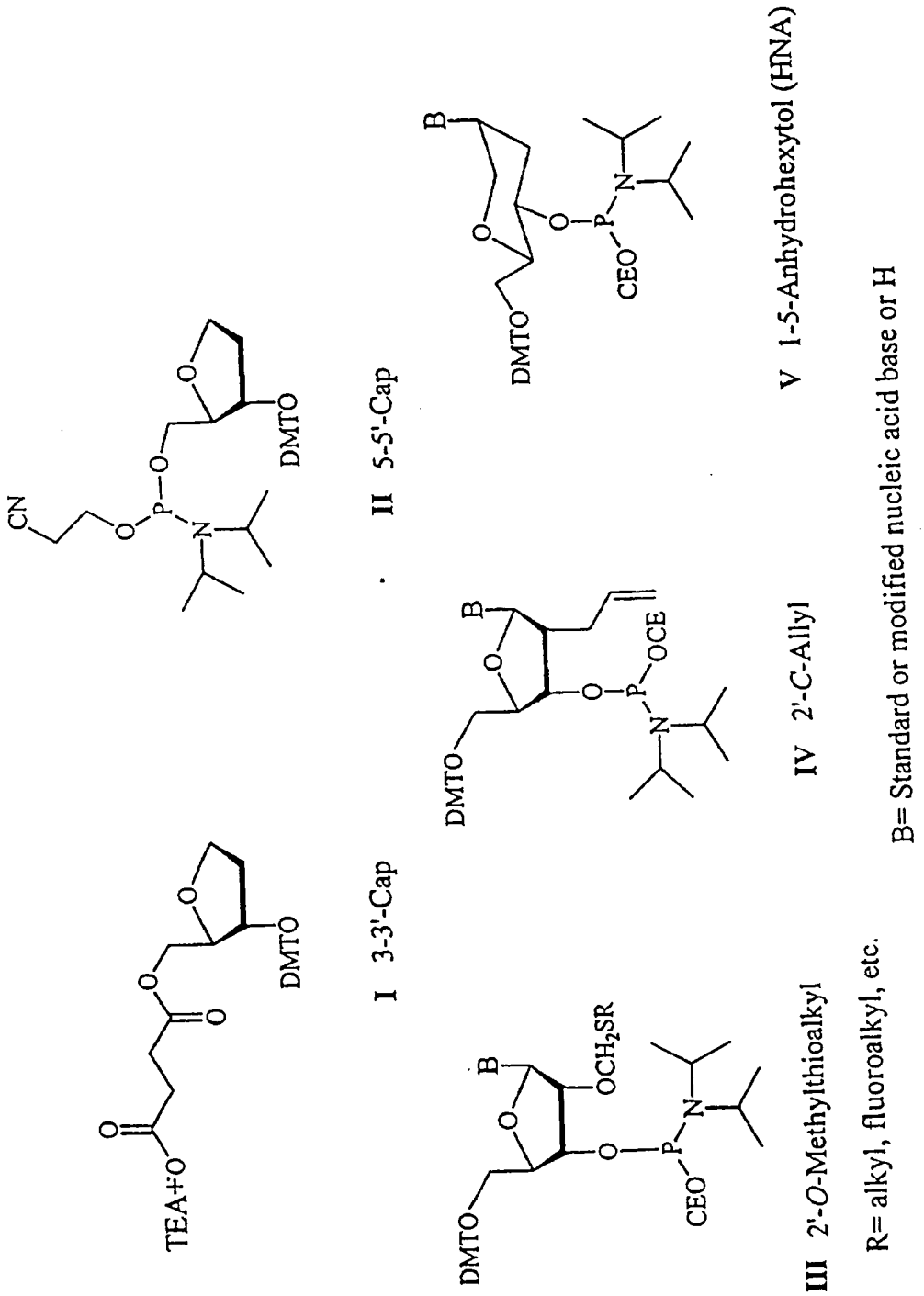

I 3-3'-Cap
II 5-5'-Cap
III 2'-O-Methylthioalkyl
IV 2'-C-Allyl
V 1-5-Anhydrohexytol (HNA)
R= alkyl, fluoroalkyl, etc.
B= Standard or modified nucleic acid base or H

Fig. 2

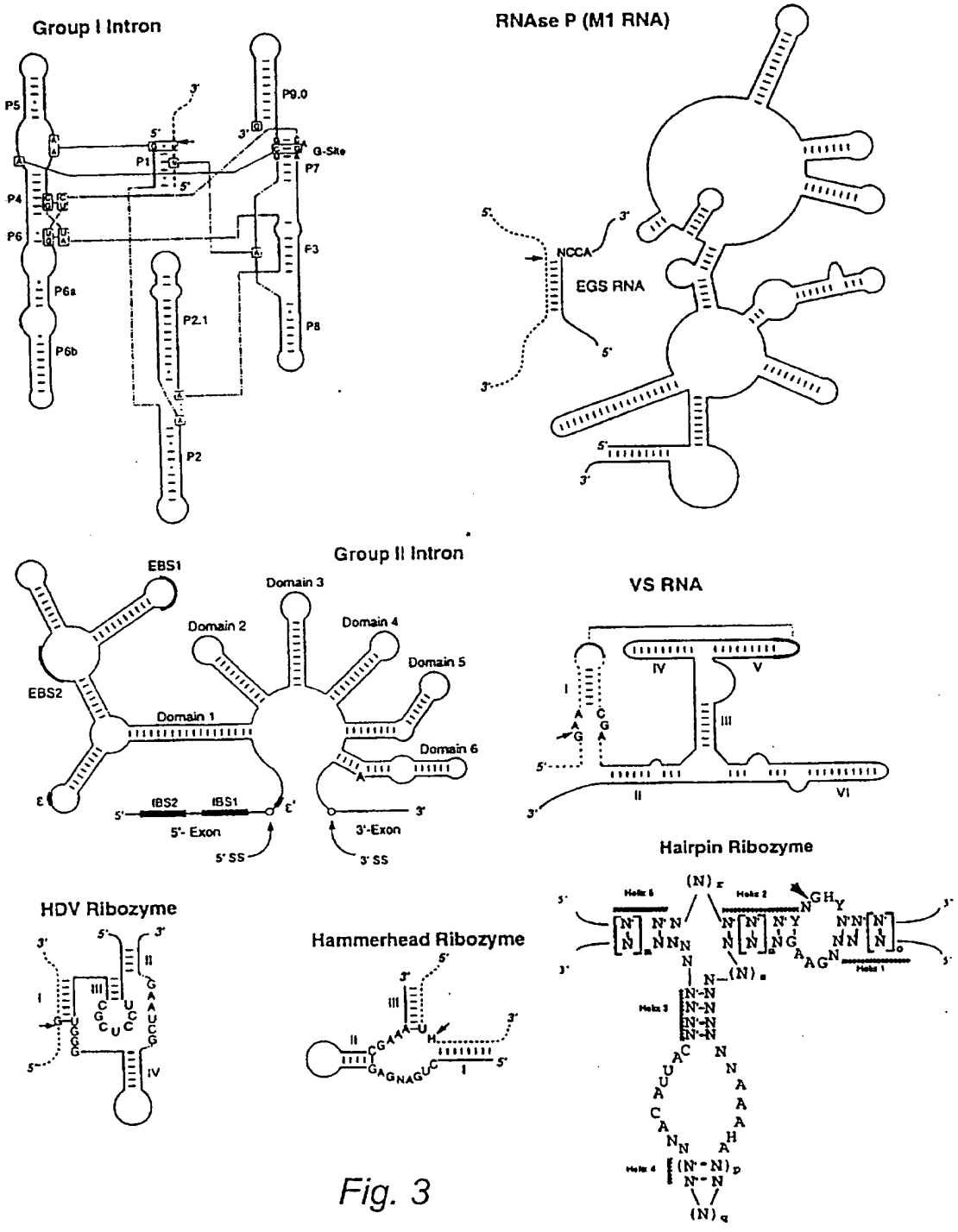

Group I Intron
P5
P9.0
P1
G-Site
P7
P4
P6
P3
P6a
P2.1
P8
P6b
P2
RNAse P (M1 RNA)
NCCA
EGS RNA
Group II Intron
EBS1
Domain 3
Domain 2
Domain 4
Domain 5
EBS2
Domain 1
Domain 6
IBS2
IBS1
5'- Exon
3'-Exon
5' SS
3' SS
VS RNA
IV
V
III
I
II
VI
HDV Ribozyme
Hammerhead Ribozyme
Hairpin Ribozyme

Fig. 3

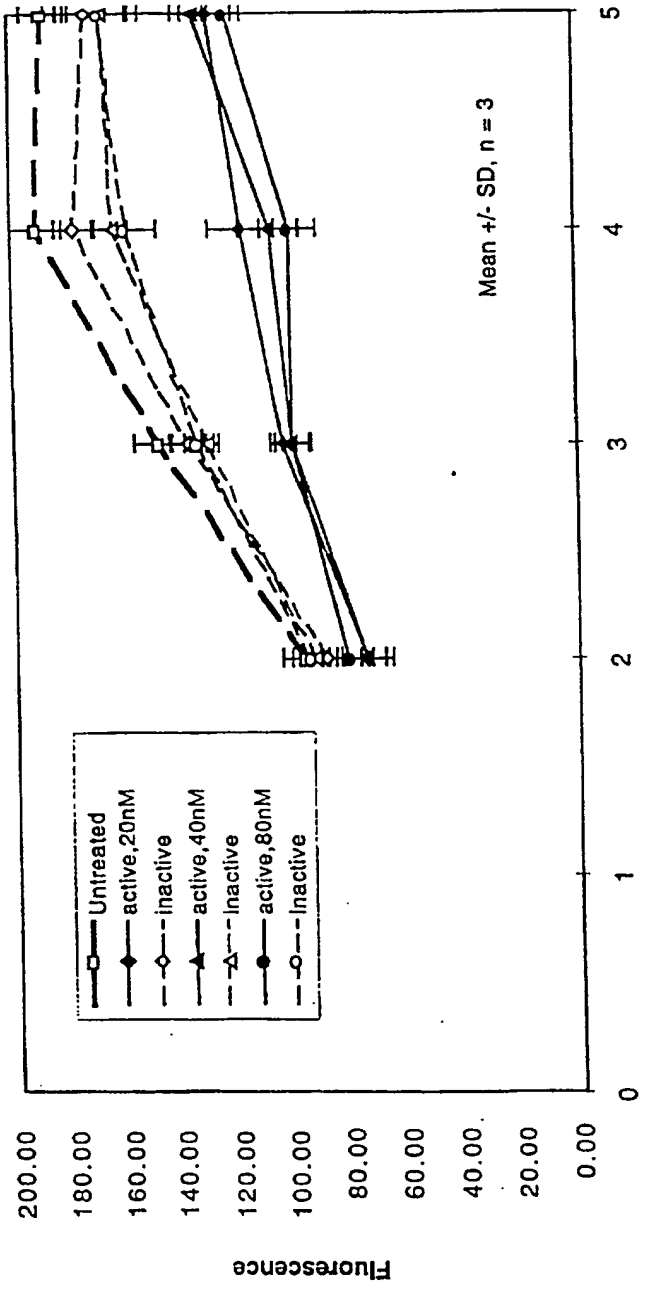

Fluorescence
200.00
180.00
160.00
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00
0
1
2
3
4
5
Days Post Treatment
Mean +/- SD, n = 3
Untreated
active,20nM
inactive
active,40nM
inactive
active,80nM
inactive

Fig. 4

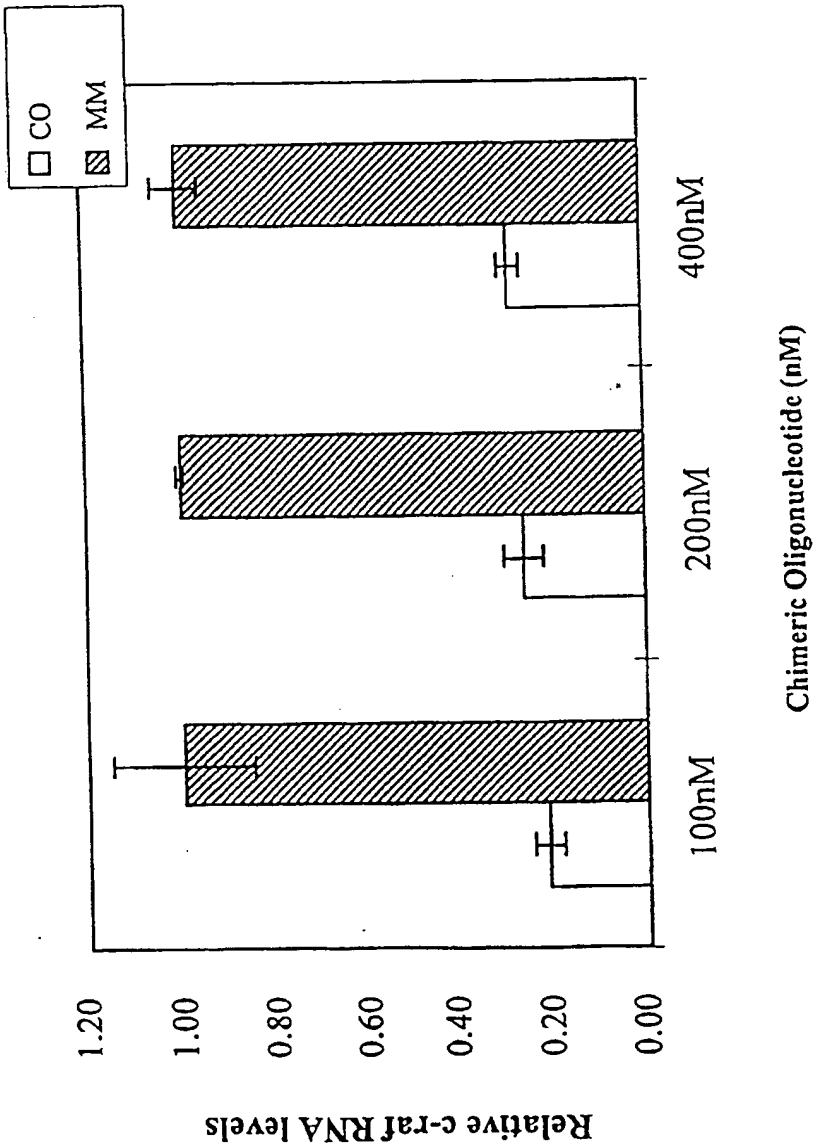

CO
MM
400nM
200nM
100nM
Chimeric Oligonucleotide (nM)
1.20
1.00
0.80
0.60
0.40
0.20
0.00
Relative c-raf RNA levels

Fig. 5

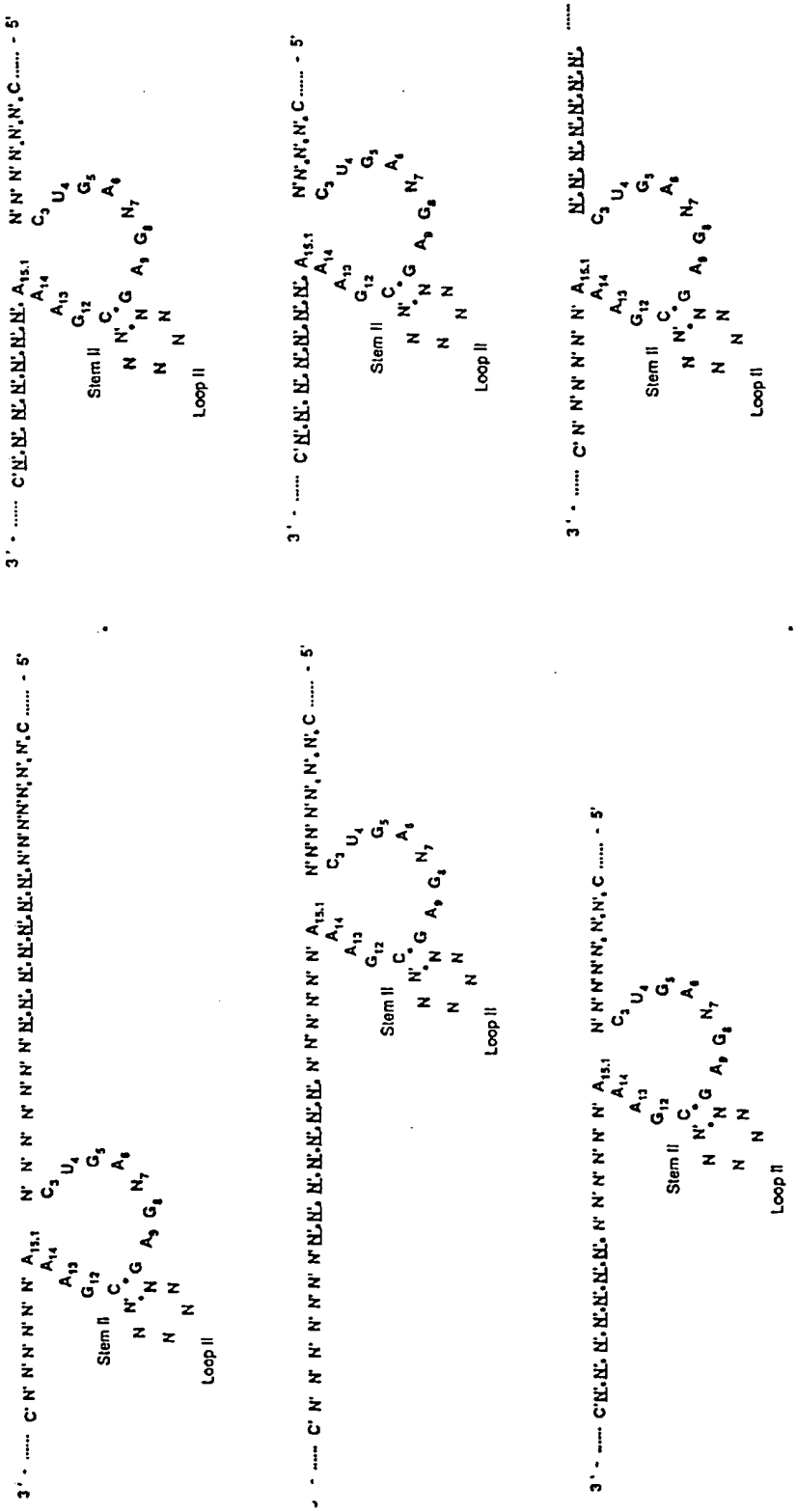

3' - ..... C' N' N' N' N' N' A15.1 N' N' N' N' N' N' N' N' N' N' N' N' N' N' N' C ..... - 5'
A14
A13
G12
C3
U4
G5
A6
Stem II
N7
N' N G A9 G8
N N
N N
Loop II

Fig. 6A

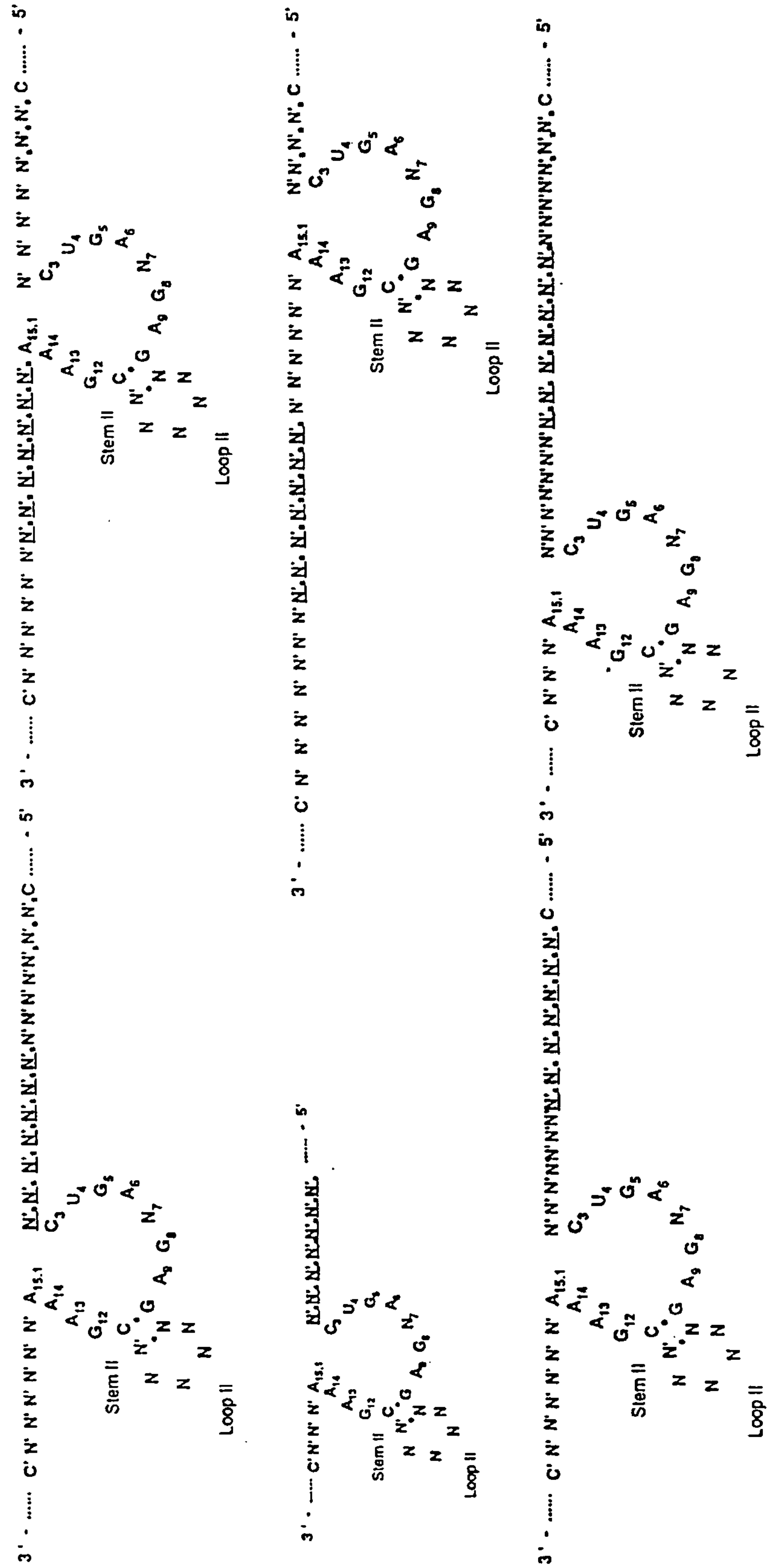


Fig. 6B

VIII
IX
X
XI
DMTO
CEO
R= H, alkyl, fluoro, amino, alkylthioalkyl,etc.
R1= alkyl, fluoroalkyl, amino, alkylthioalkyl, alkylthiofluoroalkyl, etc.
DMT or FmS
OMe
OCE
B= Standard or modified nucleic acid base or H

Fig. 7

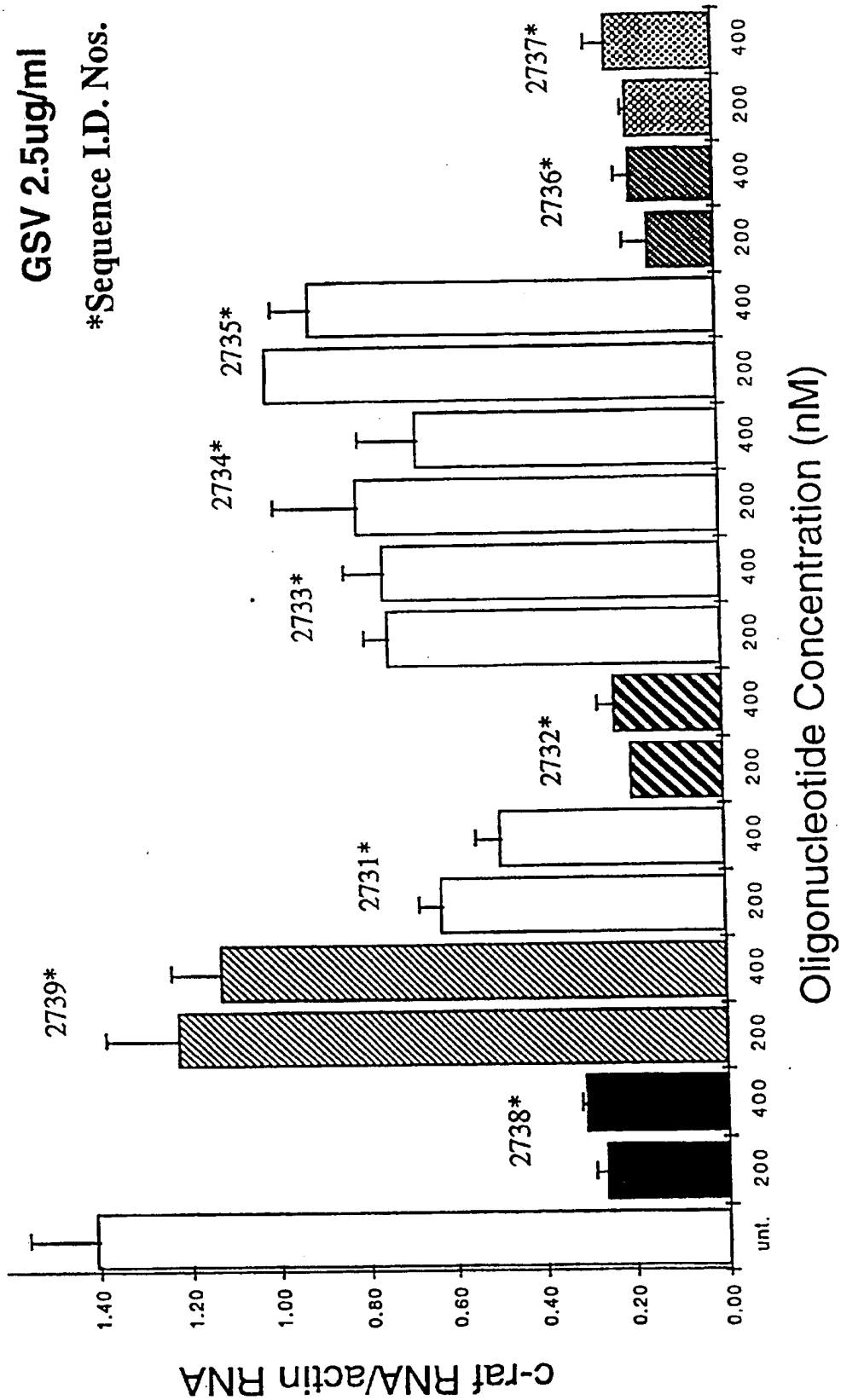

GSV 2.5ug/ml
*Sequence I.D. Nos.
c-raf RNA/actin RNA
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
unt.
200
400
2738*
2739*
2731*
2732*
2733*
2734*
2735*
2736*
2737*
Oligonucleotide Concentration (nM)

Fig. 8

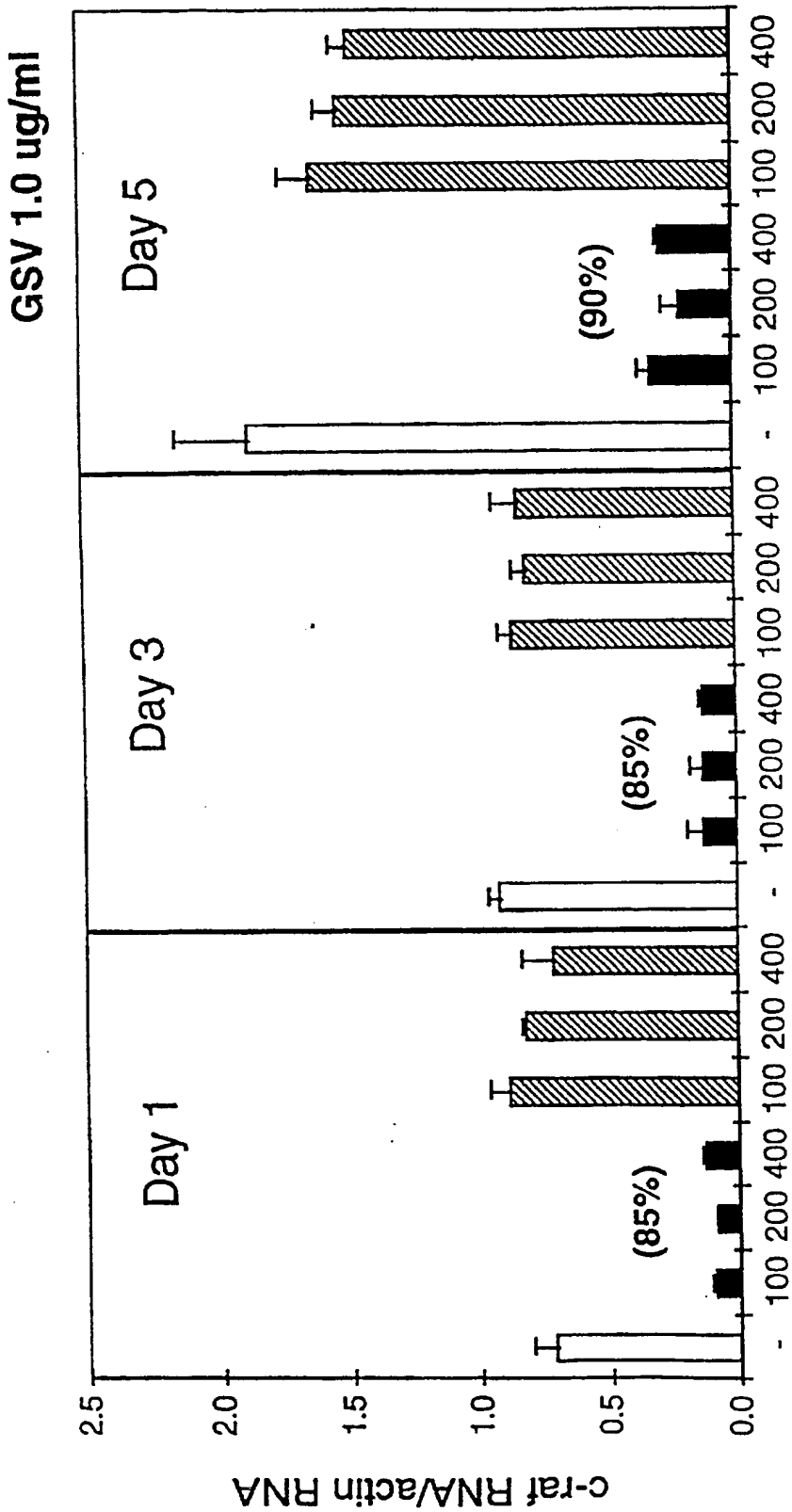

GSV 1.0 ug/ml
Day 1
Day 3
Day 5
(85%)
(85%)
(90%)
- 100 200 400 100 200 400 - 100 200 400 100 200 400 - 100 200 400
0.0
0.5
1.0
1.5
2.0
2.5
c-raf RNA/actin RNA
oligonucleotide concentration (nM)

Fig. 9

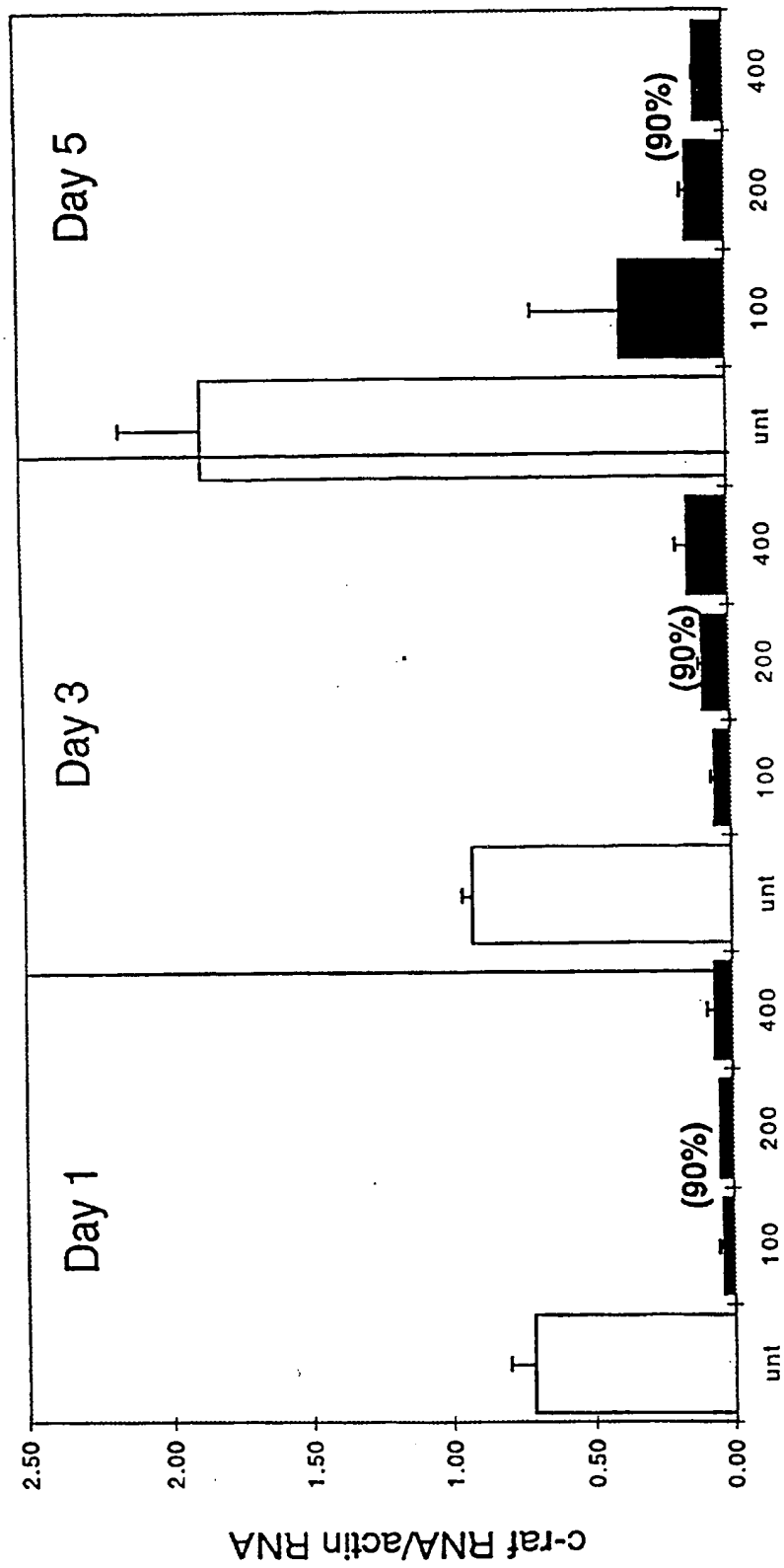

Day 1
Day 3
Day 5
(90%)
(90%)
(90%)
unt
100
200
400
unt
100
200
400
unt
100
200
400
0.00
0.50
1.00
1.50
2.00
2.50
c-raf RNA/actin RNA
oligonucleotide concentration (nM)

Fig. 10

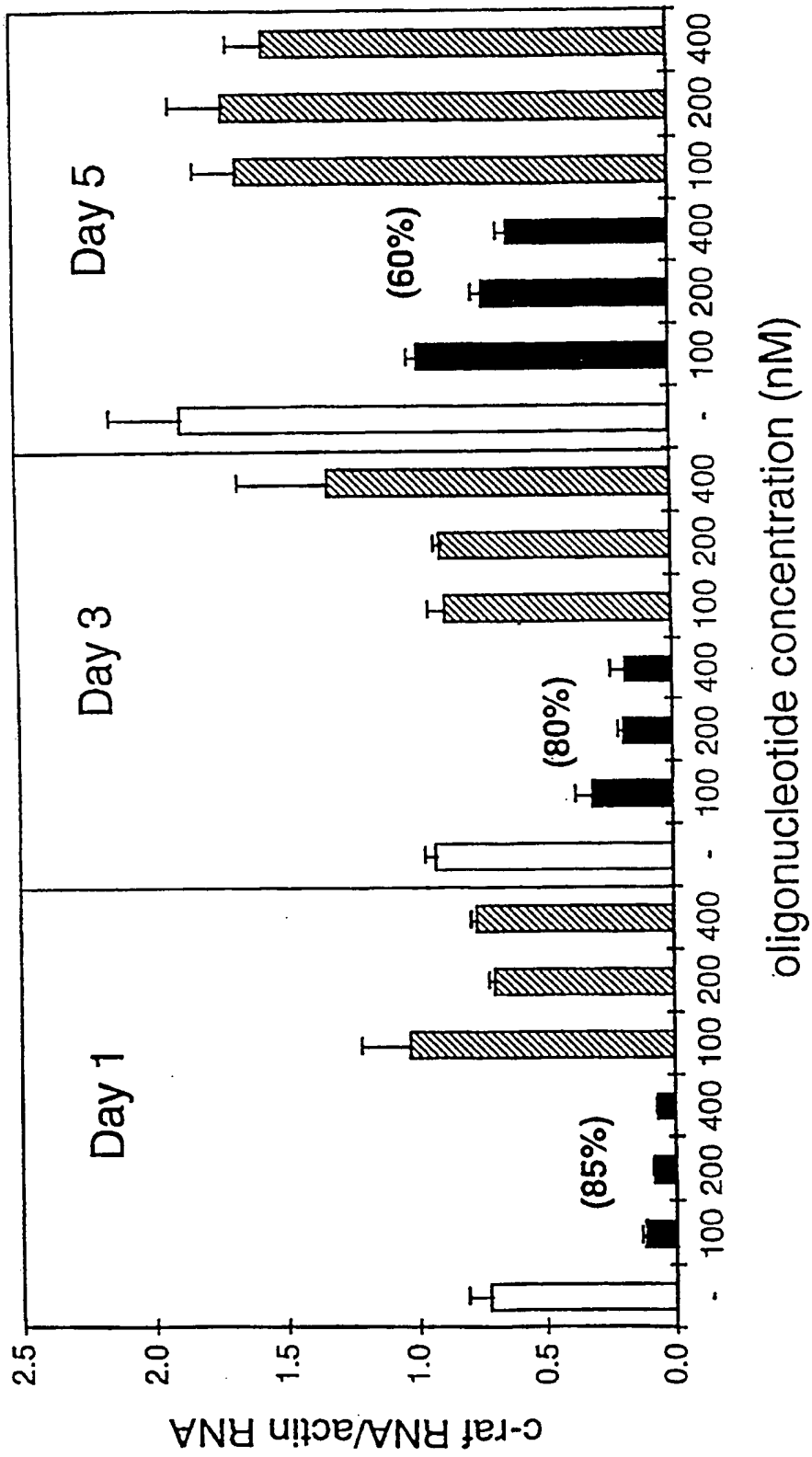

c-raf RNA/actin RNA
2.5
2.0
1.5
1.0
0.5
0.0
Day 1
Day 3
Day 5
(85%)
(80%)
(60%)
- 100 200 400 100 200 400 - 100 200 400 100 200 400 - 100 200 400 100 200 400
oligonucleotide concentration (nM)

Fig. 11

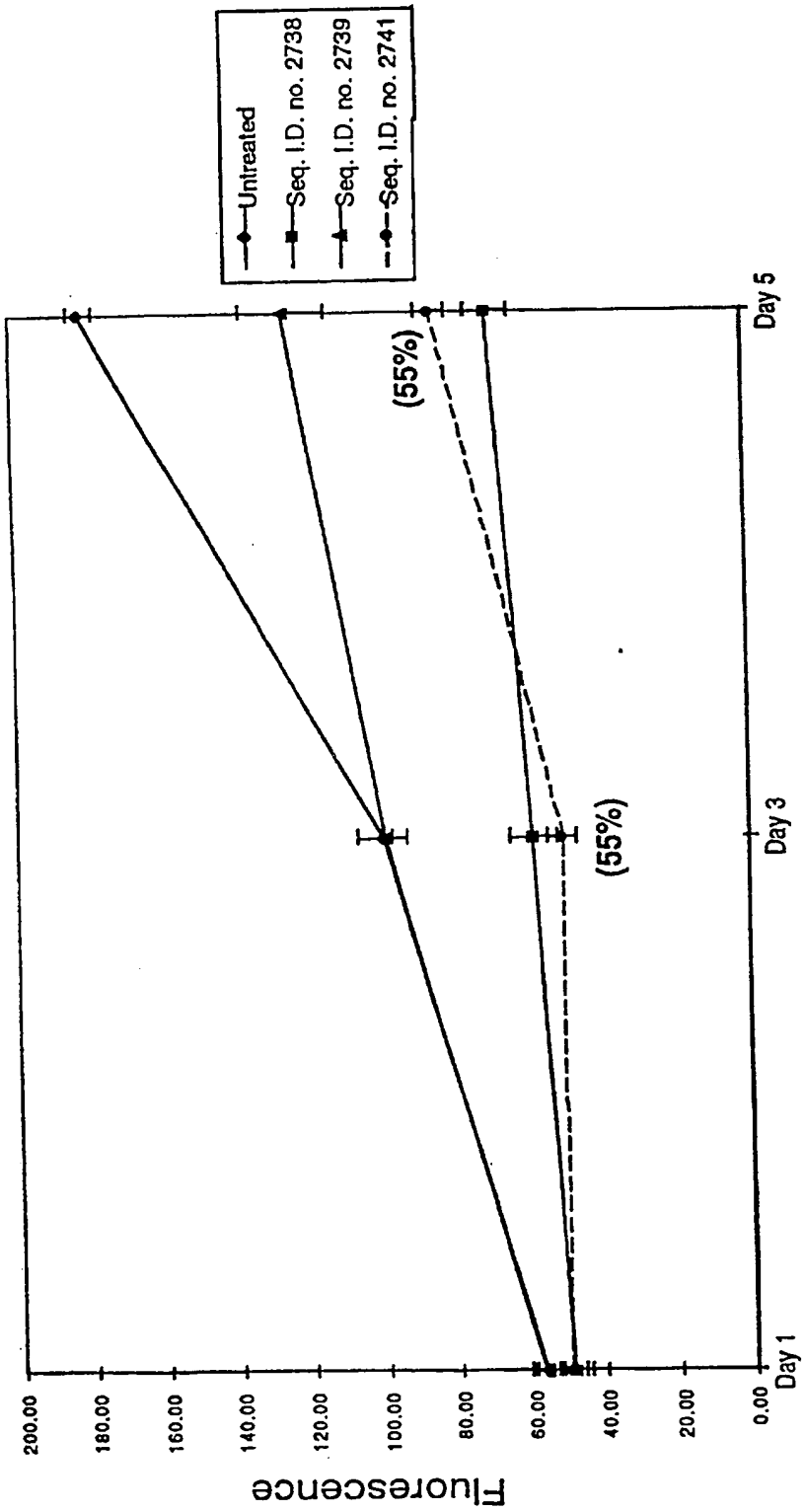

Untreated
Seq. I.D. no. 2738
Seq. I.D. no. 2739
Seq. I.D. no. 2741
(55%)
(55%)
Day 5
Day 3
Day 1
Days post treatment
Fluorescence
200.00
180.00
160.00
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00

Fig. 12

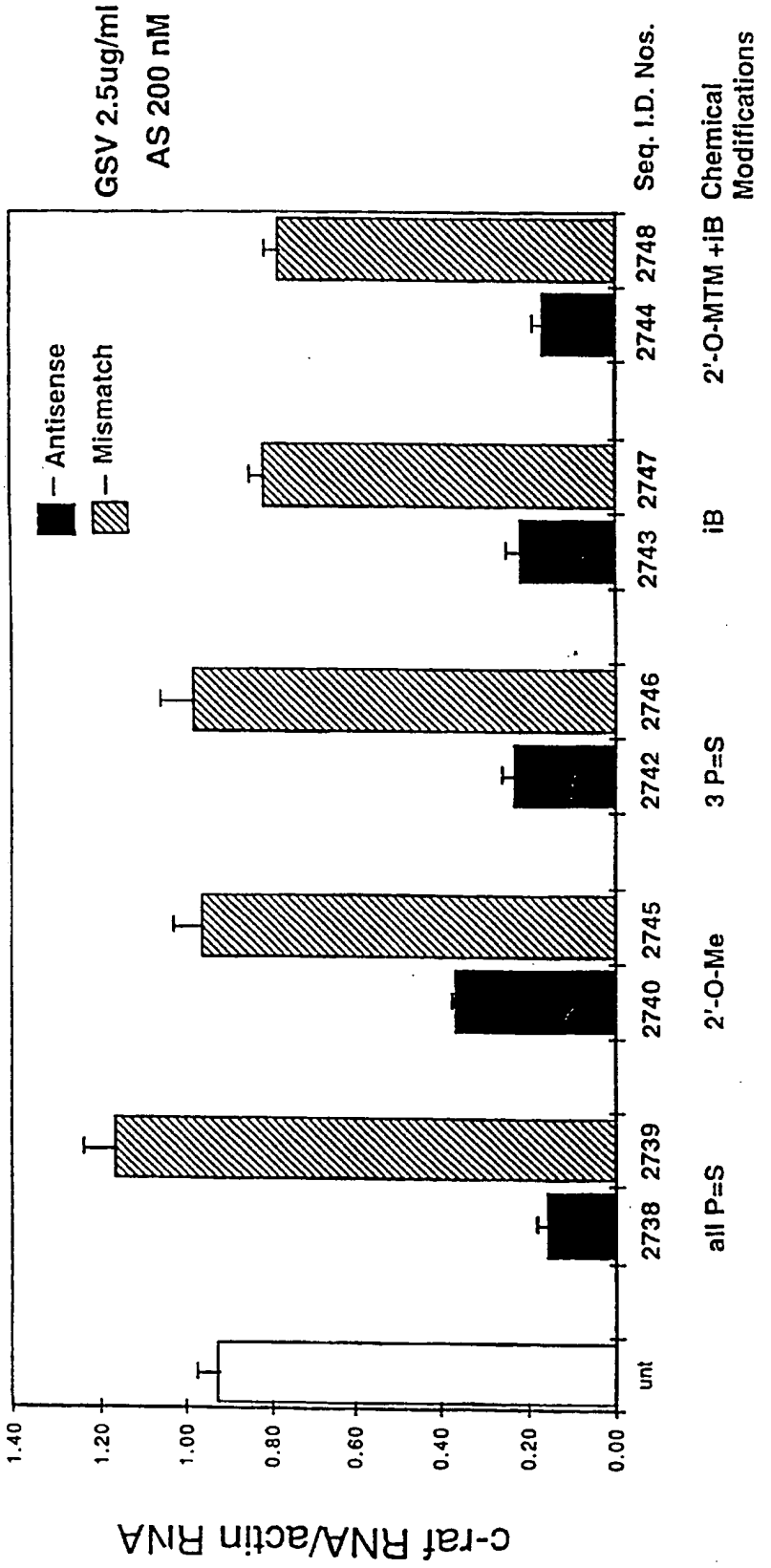

GSV 2.5ug/ml
AS 200 nM
Antisense
Mismatch
c-raf RNA/actin RNA
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
unt
2738 2739
2740 2745
2742 2746
2743 2747
2744 2748
Seq. I.D. Nos.
all P=S
2'-O-Me
3 P=S
iB
2'-O-MTM +iB
Chemical Modifications

Fig. 13

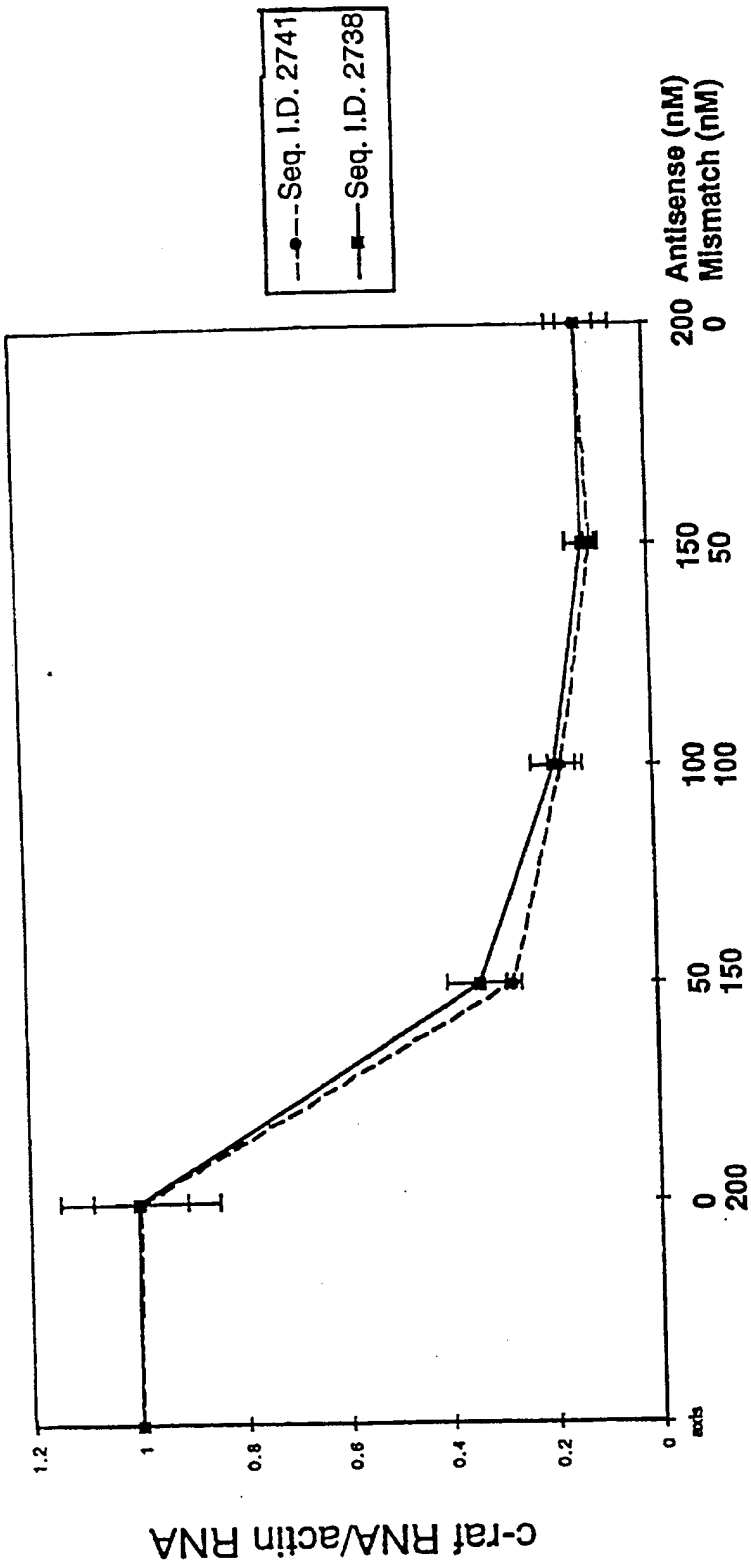

Seq. I.D. 2741
Seq. I.D. 2738
Antisense (nM)
Mismatch (nM)
200 0
150 50
100 100
50 150
0 200
c-raf RNA/actin RNA
1.2
1
0.8
0.6
0.4
0.2
0

Fig. 14

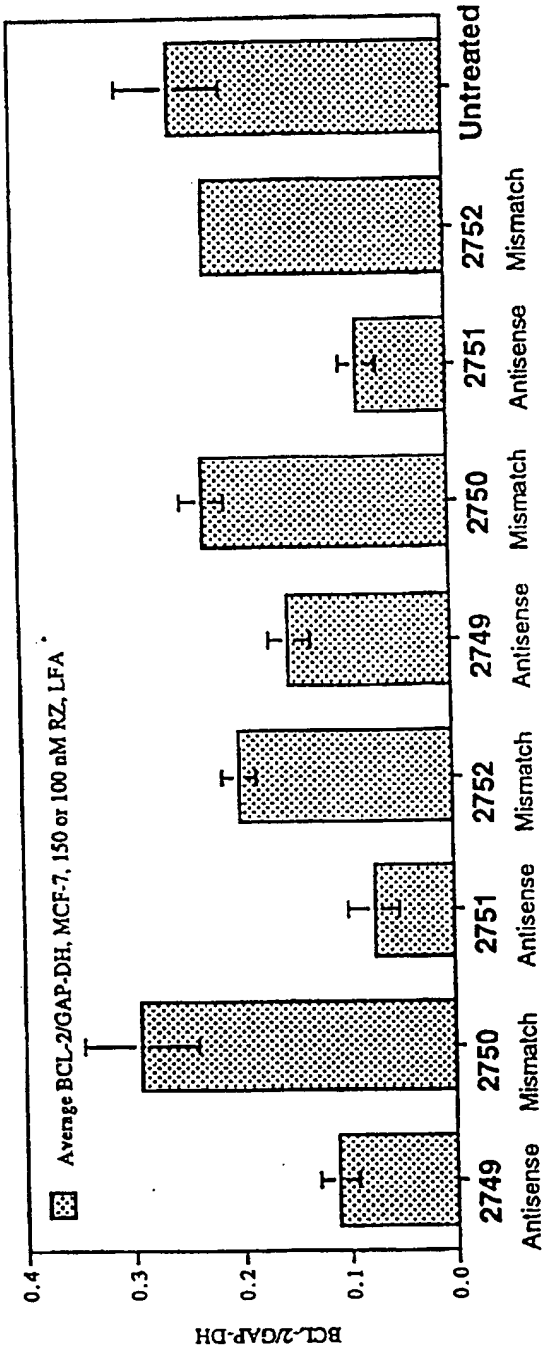

BCL-2/GAP-DH
0.0
0.1
0.2
0.3
0.4
Avenge BCL-2/GAP-DH, MCF-7, 150 or 100 nM RZ, LFA
2749 Antisense
2750 Mismatch
2751 Antisense
2752 Mismatch
2749 Antisense
2750 Mismatch
2751 Antisense
2752 Mismatch
Untreated
Seq. I.D. Nos.

Fig. 15

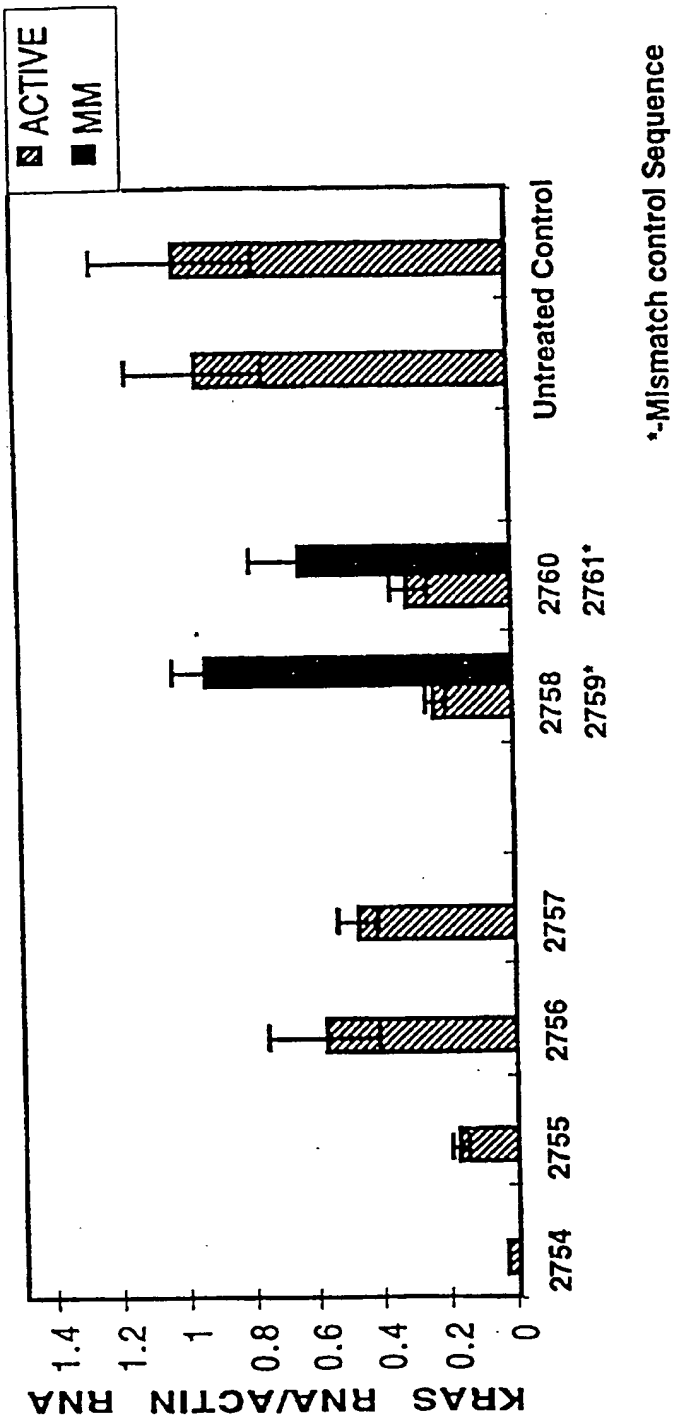

ACTIVE
MM
KRAS RNA/ACTIN RNA
1.4
1.2
1
0.8
0.6
0.4
0.2
0
2754
2755
2756
2757
2758
2759*
2760
2761*
Untreated Control
*-Mismatch control Sequence
Sequence I.D. Nos.

Fig. 16

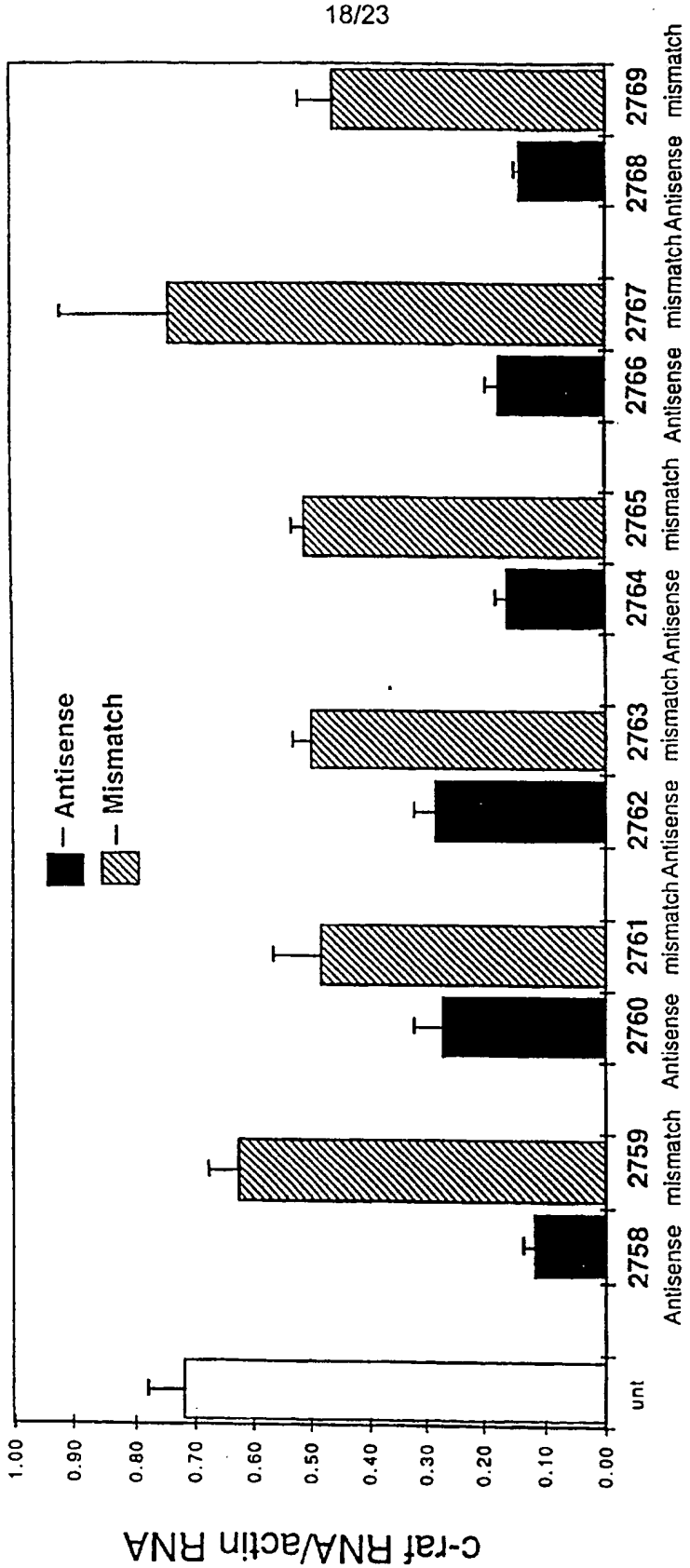
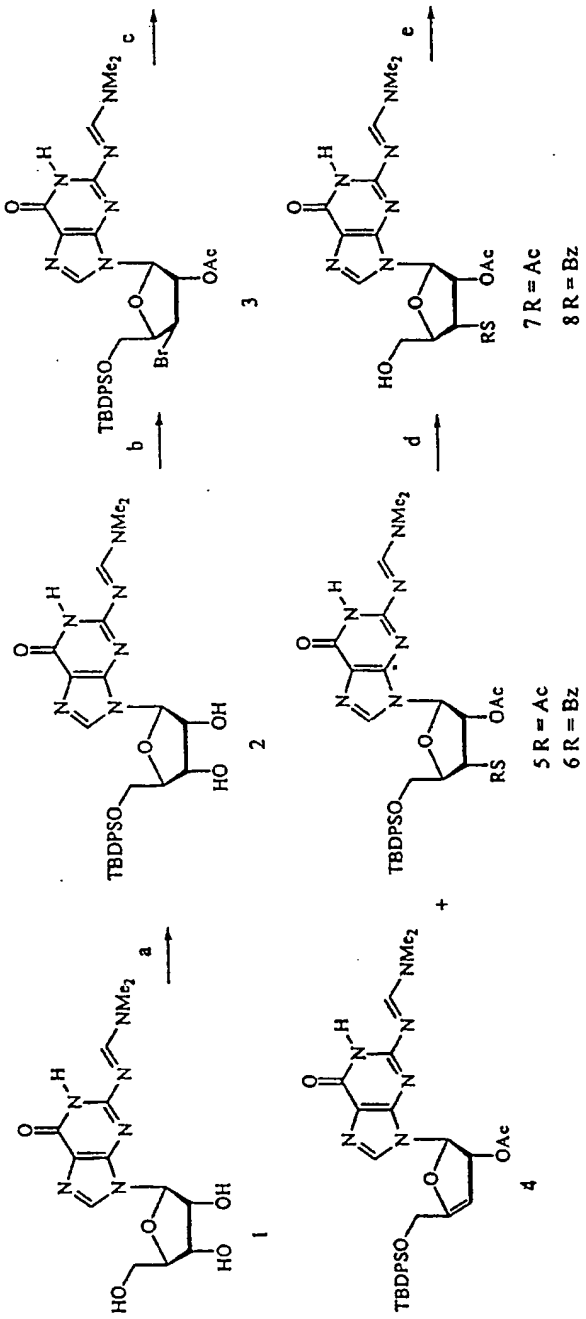
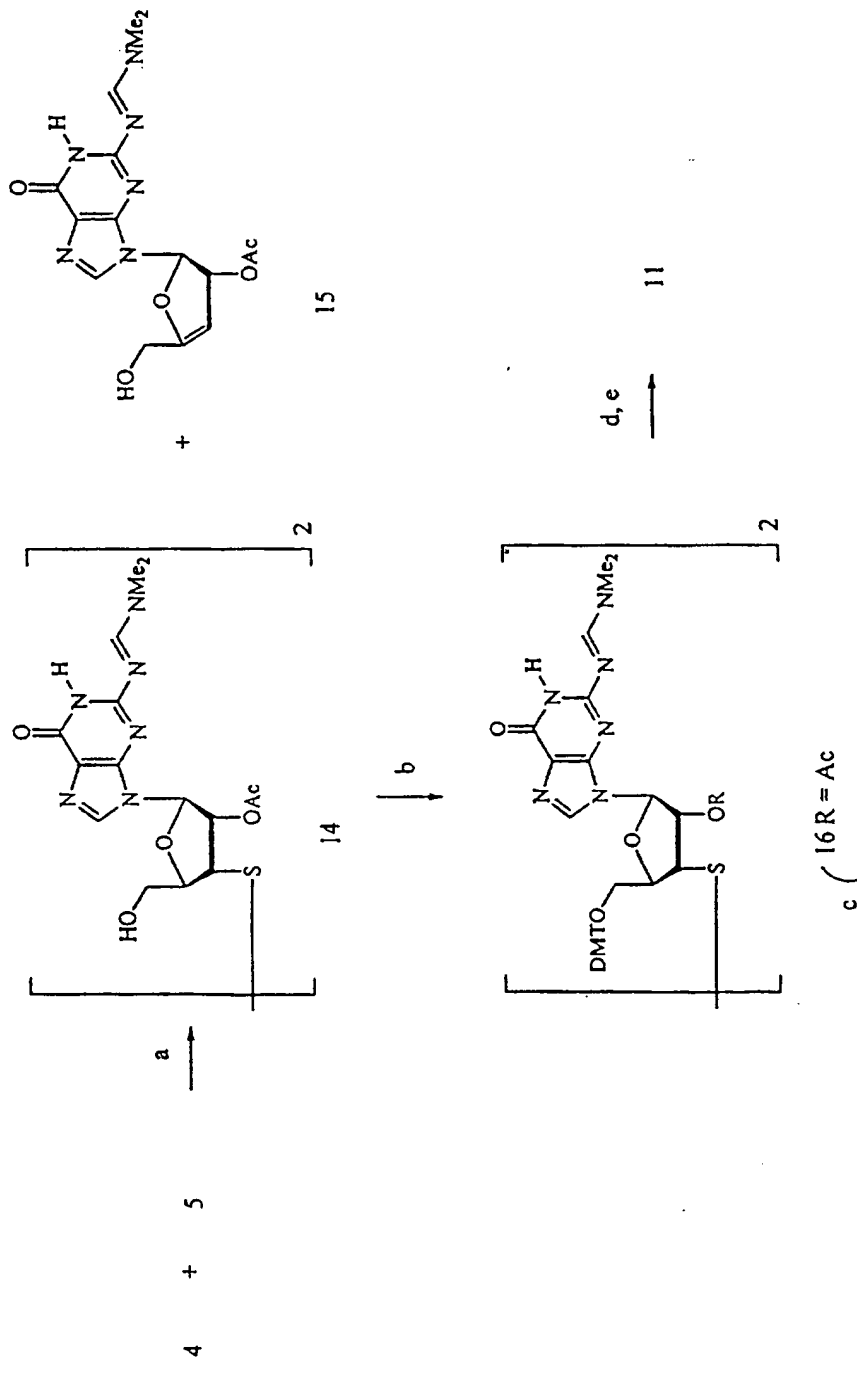

c-raf RNA/actin RNA
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
Antisense
Mismatch
unt
2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769
Antisense mismatch Antisense mismatch Antisense mismatch Antisense mismatch Antisense mismatch
Seq. I.D. Nos.

Fig. 17



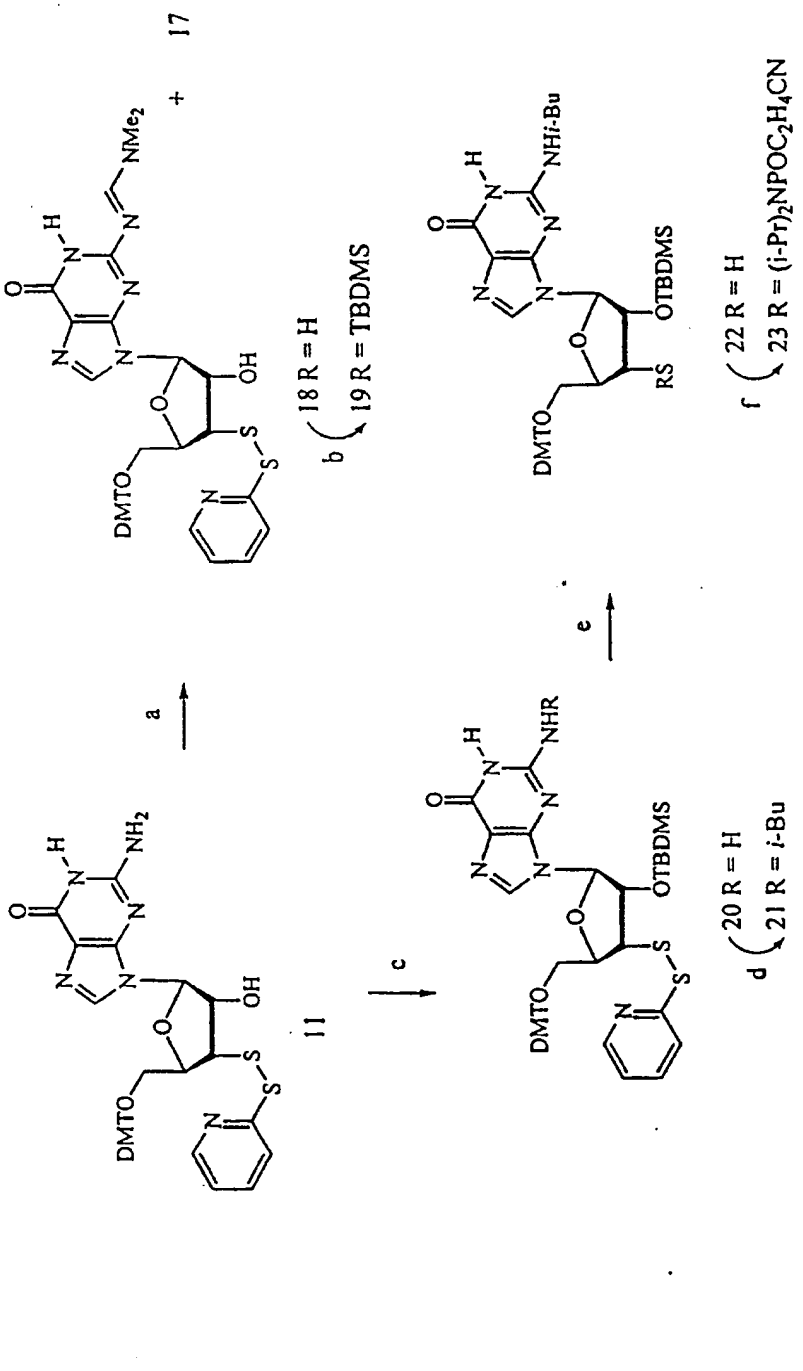
Reagents and conditions: (a) TBDPS-Cl, Pyr, rt, 16 h: (b) $Me_2C(OAc)COBr$, MeCN, H_2O, rt, 3 h; (c) KSAc or KSBz, DMF, 60 °C, 10 h; (d) $TBAF \cdot 3H_2O$, AcOH, THF, rt, 5 h; (e) DMT-Cl, Pyr, rt, 4 h; (f) 40% aq.$MeNH_2$, rt, 16 h; (g) 2,2'-dipyridyl disulfide, DMF, 60 °C, 10 h; (i) DTT, $CHCl_3$, rt, 3 h; (j) 1N HCl in MeOH, DTT, rt, 3 h.

Fig. 18



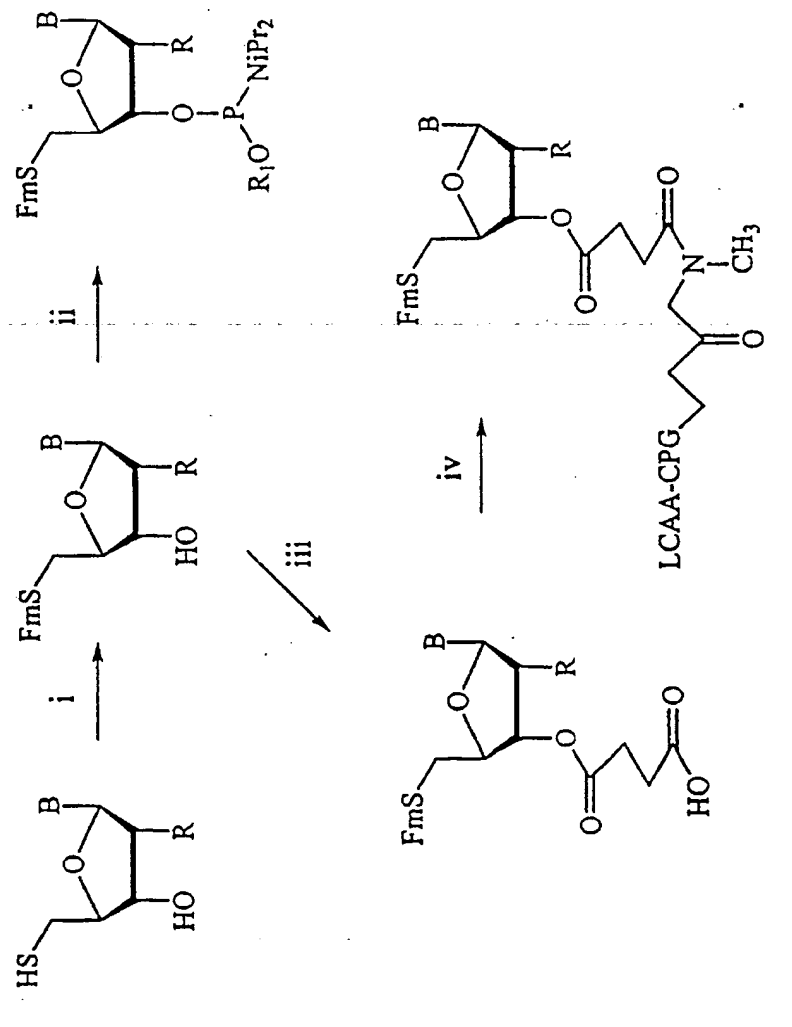
Reagents and conditions: (a) 1 M TBAF in THF, rt, 3 h; (b) DMT-Cl, Pyr, rt, 4 h; (c) 1E AG1X8 (OH^-) or Amberlyst A-26 (CN^-); MeOH, 55 °C, 16 h; (d) 40% aq. $MeNH_2$, rt, 16 h; (e) 2,2'-dipyridyl disulfide, DMF, 60 °C, 10 h.

Fig. 19



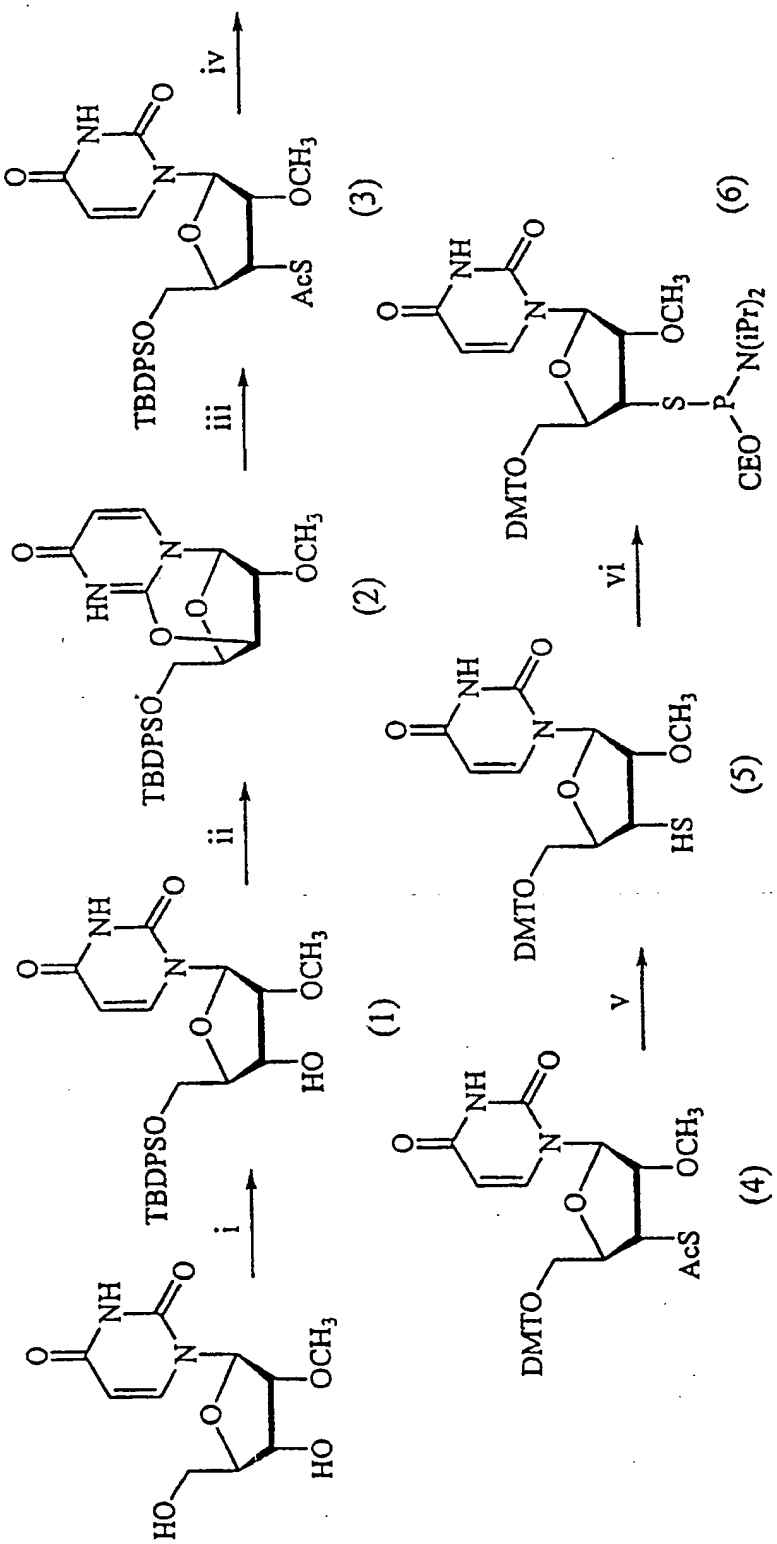
Reagents and conditions: (a) $Me_2NCH(OMe)_2$, Pyr, rt, 16 h; (b) TBDMS-Tf, Pyr, rt, 5 h; (c) TBDMS-Cl, Pyr, Im, rt, 16 h; (d) i-Bu_2O, Pyr, DMAP, rt, 16 h, then 50 °C, 5 h; (e) DTT, $CHCl_3$, TEA; (f) $(i\text{-}Pr)_2NP(Cl)OC_2H_4CN$, DIPEA, 1-MeIm, rt, 2 h.

Fig. 20



Reagents: (i) fluorenylmethyl chloride, DIEA, DMF or DCM; (ii) 2-cyanoethyltetraisopropylchlorophosphoro-diamidite (for R_1 = cyanoethyl) or methyltetraisopropylchlorophosphorodiamidite (for R_1 = Me), tetrazole; (iii) succinic anhydride, DMF; (iv) CH_3NH-CH_2CONH-LCAA-CPG, DCC.

Fig. 21



i. TBDPSCl/pyridine
ii. PPh_3, DEAD/THF
iii. thioacetic acid
iv. a. TBAF/THF/HOAC b. DMTCl/pyridine
v. MeNH2, DTT
vi. standard conditions

Fig. 22